

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 03:38:41 ; Search time 21 Seconds
(without alignments)
1055.099 Million cell updates/sec

Title: US-10-089-485-4

Perfect score: 268

Sequence: 1 MSLSFLLLFFSHLLISAWA.....LSAPKNTMSVYKRLKFRG 268

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pep:*\n2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*\n3: /cgn2_6/prodata/1/iaa/8 COMB.pep:*\n4: /cgn2_6/prodata/1/iaa/PCUS COMB.pep:*\n5: /cgn2_6/prodata/1/iaa/IB COMB.pep:*\n6: /cgn2_6/prodata/1/iaa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	100.0	268	1	US-08-439-725A-12 Sequence 12, Appl
2	268	100.0	268	1	US-08-464-590A-17 Sequence 17, Appl
3	268	100.0	268	1	US-08-207-412B-12 Sequence 12, Appl
4	268	100.0	268	1	US-08-867-471-12 Sequence 12, Appl
5	268	100.0	268	1	US-08-438-439C-8 Sequence 8, Appl
6	268	100.0	268	1	US-08-951-822-33 Sequence 33, Appl
7	268	100.0	268	2	US-08-718-904-14 Sequence 14, Appl
8	268	100.0	268	2	US-09-093-585-17 Sequence 17, Appl
9	268	100.0	268	2	US-09-368-951-33 Sequence 33, Appl
10	268	100.0	268	2	US-09-449-249-14 Sequence 14, Appl
11	268	100.0	268	2	US-09-990-207-20 Sequence 20, Appl
12	268	100.0	268	2	US-09-329-947-33 Sequence 33, Appl
13	268	100.0	268	2	US-09-572-406B-11 Sequence 11, Appl
14	226	84.3	247	2	US-09-240-952-5 Sequence 5, Appl
15	226	84.3	248	2	US-09-240-952-3 Sequence 3, Appl
16	226	84.3	268	2	US-09-023-082A-15 Sequence 15, Appl
17	226	84.3	268	2	US-09-240-952-2 Sequence 2, Appl
18	226	84.3	268	2	US-09-248-998-15 Sequence 15, Appl
19	226	84.3	268	2	US-09-610-651-15 Sequence 15, Appl
20	226	84.3	268	2	US-09-345-373-15 Sequence 15, Appl
21	226	84.3	268	2	US-10-075-446-15 Sequence 15, Appl
22	198	73.9	268	1	US-08-438-439C-18 Sequence 18, Appl
23	195	72.8	268	2	US-09-949-016-7942 Sequence 7942, Ap
24	182	67.9	266	1	US-09-417-721-15 Sequence 15, Appl
25	182	67.9	267	2	US-08-462-169B-13 Sequence 13, Appl
26	182	67.9	267	2	US-09-103-079-13 Sequence 13, Appl
27	182	67.9	267	2	US-09-425-021-13 Sequence 13, Appl

28	182	67.9	267	2	US-09-564-829-7 Sequence 7, Appl
29	172	64.2	219	1	US-08-441-629-13 Sequence 13, Appl
30	172	64.2	219	2	US-08-776-207-13 Sequence 13, Appl
31	172	64.2	219	2	US-09-507-773-13 Sequence 13, Appl
32	172	64.2	219	2	US-10-016-447-13 Sequence 13, Appl
33	172	64.2	219	4	PCR-US95-09172-13 Sequence 9, Appl
34	151	56.3	266	2	US-09-417-721-9 Sequence 9, Appl
35	151	56.3	268	2	US-08-705-245-14 Sequence 14, Appl
36	151	56.3	268	2	US-09-490-714-14 Sequence 14, Appl
37	119	44.4	123	1	US-08-822-573-2 Sequence 2, Appl
38	90	33.6	266	6	US-08-822-573-2 Sequence 30, Appl
39	50	18.7	266	6	5175383-5 Patent No. 5175383
40	39	14.6	121	1	US-08-822-573-4 Sequence 4, Appl
41	27	10.1	27	1	US-08-290-373B-6 Sequence 6, Appl
42	15	5.6	15	2	US-09-537-817B-1 Sequence 1, Appl
43	15	5.6	19	2	US-09-537-817B-10 Sequence 10, Appl
44	13	4.9	13	2	US-09-537-817B-9 Sequence 9, Appl
45	11	4.1	15	2	US-09-537-817B-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-439-725A-12
Sequence 12, Application US/08439725A
Patent No. 5693775
GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSER: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,725A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/047001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 617/678-5099
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-439-725A-12
Query Match 100.0%; Score 268; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.6e-244; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0;
OY 1 MSLSFLLLFFSHLLISAWAGEKRLAPKGPATPDNRNPISGSSRSSSSAMSSSSAS 60
DB 1 MSLSFLLLFFSHLLISAWAGEKRLAPKGPATPDNRNPISGSSRSSSSAMSSSSAS 60

QY 61 SSPASISGSGLEQSSPQSPSGRRTSLYCRVIGIHLQIYDPGKXGSHANMLSV 120
DB 61 SSPASISGSGGLEQSSPQSPSGRRTSLYCRVIGIHLQIYDPGKXGSHANMLSV 120
QY 121 LEIFAVSQIGIRGVSNKFLAMSKKGLHASAKFTDDCKFRERFQENSNTYVSAIHR 180
DB 121 LEIFAVSQIGIRGVSNKFLAMSKKGLHASAKFTDDCKFRERFQENSNTYVSAIHR 180
QY 181 TEKTRERWVALANKGKAKRGCSPRVKPOHISTHFLPRKQSEBPELSTYTVVPEKKNP 240
DB 181 TEKTRERWVALANKGKAKRGCSPRVKPOHISTHFLPRKQSEBPELSTYTVVPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 2
US-08-464-590A-17
Sequence 17, Application US/08464590A
Patent No. 5763214
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: US
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,590A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J. G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1700
TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-590A-17

Query Match 100.0%; Score 268; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.6e-244;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 LEIFAVSQIGIRGVSNKFLAMSKKGLHASAKFTDDCKFRERFQENSNTYVSAIHR 180
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DB 181 TEKTRERWVALANKGKAKRGCSPRVKPOHISTHFLPRKQSEBPELSTYTVVPEKKNP 240
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DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 3
US-08-207-412B-12
Sequence 12, Application US/08207412B
Patent No. 5817485
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
TITLE OF INVENTION: Fibroblast Growth Factor-10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,412B
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petrarro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-207-412B-12

Query Match 100.0%; Score 268; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.6e-244;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 33, Application US/08951822A
; Patent No. 5989866
; GENERAL INFORMATION:
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Raymond, Fenella
; APPLICANT: Bukowski, Thomas R.
; APPLICANT: Holderman, Susan D.
; APPLICANT: Hansen, Birgit
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
; FILE REFERENCE: 96-20
; CURRENT APPLICATION NUMBER: US/08/951,822A
; CURRENT FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 3.10
; SEQ ID NO 33
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-951-822-33

Query Match 100.0%; Score 268; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.6e-244;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 SPIKSKIPLSAPRKNTNSVYKRLKFRFG 268
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RESULT 7
US-08-718-904-14
; Sequence 14, Application US/08718904
; Patent No. 6037329
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037329tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.415C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: /note= "FGF-5"
US-08-718-904-14

Query Match 100.0%; Score 268; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.6e-244;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SSPASLSGSGSGLEQSSFFQWSPSGRTGSLYCRVIGFHLQIYPDGKNGSHEANMLSV 120
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DB 121 LEIFAVSGIIVIGRVFVNKFLAMSKGKGLHASAKFTDDCKFRERFQENSYNTYASAIHR 180
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DB 181 TEKTRGVYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEBELSFTYVPEKKNP 240
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DB 241 SPIKSKIPLSAPRKNTNSVYKRLKFRFG 268

RESULT 8
US-09-093-585-17
; Sequence 17, Application US/09093585
; Patent No. 6110893
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NJ
; COUNTRY: US
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,585
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/464,590
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:


```

? NAME: MULLINS, J. G.
? REGISTRATION NUMBER: 30,073
? REFERENCE/DOCKET NUMBER: 325800-438
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (201) 994-1700
? TELEFAX: (201) 994-1744
? INFORMATION FOR SEQ ID NO: 17:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 268 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?-
?-JS-093-585-17

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Query Match	100.0%;	Score 268;	DB 2;	Length 268;
Best Local Similarity	100.0%;	Pred. NO. 6.6e-24;		
Matches 268; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

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Db	1	MSLSFLLLLFFSHLLISAMAHGEKRLAPGQGPATDRNPITGSSSRSSSSAMSSAS	60
Qy	61	SSPAASISGSGSLGEBSSFWMPSPGRRTSLSYCRVIGIGHLIQYDCKVNGSHEANLSTV	120
Db	61	SSPAASISGSGSLGEBSSFWMPSPGRRTSLSYCRVIGIGHLIQYDCKVNGSHEANLSTV	120
Qy	121	LEIFAVSQGI VGI RGVFSNKF LAMS KKGGLHLSAFTDDCKFRBRFOENSNYNTASA IHR	180
Qy	121	LEIFAVSQGI VGI RGVFSNKF LAMS KKGGLHLSAFTDDCKFRBRFOENSNYNTASA IHR	180
Db	121	LEIFAVSQGI VGI RGVFSNKF LAMS KKGGLHLSAFTDDCKFRBRFOENSNYNTASA IHR	180
Qy	181	TEKTGNBYVALNKRKAKARGCSPRYKPOHISTHFLPRPKOSEDELSFTVVEKQNP	240
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Db	181	TEKTGNBYVALNKRKAKARGCSPRYKPOHISTHFLPRPKOSEDELSFTVVEKQNP	240
Qy	241	SPITSKTIPLSAPRKNTNSVYTKLKPFEG	268
Qy	241	SPITSKTIPLSAPRKNTNSVYTKLKPFEG	268
Db	241	SPITSKTIPLSAPRKNTNSVYTKLKPFEG	268

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RESULTS 9
US-09-368-951-33
; Sequence 33, Application US/09368951
; Patent No. 6352971
; GENERAL INFORMATION:
; APPLICANT: Deistner, Theresa A.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Raymond, Fenella
; APPLICANT: Bukowski, Thomas R.
; APPLICANT: Holderman, Susan D.
; APPLICANT: Hansen, Birgit
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
; FILE REFERENCE: 96-20
; CURRENT APPLICATION NUMBER: US/09/368,951
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 08/951,822
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0.
; SEQ ID NO 33
; LENGTH: 268
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-368-951-33

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Query Match      100.0% Score 268; DB 2; Length 268;
Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1 MSLSFLLLPFSHLLLSAMANGEKRIAPKGPDPATDNNPTGSSRGSSSAMSSSSAS 60
Db      1 MSLSFLLLPFSHLLLSAMANGEKRIAPKGPDPATDNNPTGSSRGSSSAMSSSSAS 60

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Oy	121	LBIPAVSOGIVIGIRGVSNKFLAMSKKGLHSAKAFKTDCKFRBRPOENSINTYASA1HR	180
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Oy	181	TEXTGHEWYVALLNKRKGAKARCGSPRVKQOH1STHPLPRKSOBOPHLSFTYTVBEKONPP	240
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1      RESULT 10
2      US-09-449-249-14
3      : Sequence 14, Application US/09449249
4      : Patent No. 650386
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Baird, J. Andrew
8      :               Chandler, Lois Ann
9      :               Sosnowski, Barbara A.
10     : TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THER
11     : NUMBER OF SQUENCES: 128
12     : CORRESPONDENCE ADDRESS:
13     : ADDRESSEE: SEED and BERRY LLP
14     : STREET: 6300 Columbia Center, 701 Fifth Avenue
15     : CITY: Seattle
16     : STATE: Washington
17     : COUNTRY: USA
18     : ZIP: 98104-7092
19     :
20     : COMPUTER READABLE FORM:
21     : MEDIUM TYPE: Floppy disk
22     : COMPUTER: IBM PC compatible
23     : OPERATING SYSTEM: PC-DOS/MS-DOS
24     : SOFTWARE: Patent In Release #1.0, Version #1.25
25     :
26     : CURRENT APPLICATION DATA:
27     : APPLICATION NUMBER: US/09/449,249
28     : FILING DATE: 24-No. 6503886-1999
29     : CLASSIFICATION: <Unknown>
30     :
31     : PRIOR APPLICATION DATA:
32     : APPLICATION NUMBER: US/08/718,904
33     : FILING DATE: 24-SEP-1996
34     :
35     : ATTORNEY/AGENT INFORMATION:
36     : NAME: No. 650386tendura Ph.D., Carol
37     : REGISTRATION NUMBER: 39,317
38     : REFERENCE/DOCKET NUMBER: 760100.41SC1
39     : TELECOMMUNICATION INFORMATION:
40     : TELEPHONE: (206) 622-4900
41     : TELEFAX: (206) 682-6031
42     :
43     : INFORMATION FOR SEQ ID NO: 14:
44     : SEQUENCE CHARACTERISTICS:
45     : LENGTH: 268 amino acids
46     : TYPE: amino acid
47     : STRANDEDNESS: single
48     : TOPOLOGY: unknown
49     : MOLECULE TYPE: peptide
50     :
51     : FEATURE:
52     : OTHER INFORMATION: /note= "FGF-5"
53     :
54     : SEQUENCE DESCRIPTION: SEQ ID NO: 14:
55     :
56     : US-09-449-249-14

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Query Match Similarity	100.0%	Score 268	DB 2	Length 268
Best Local Similarity	100.0%	Pred. No. 6.6e-244		
Matches 268	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MSLSFLLLPFSSHILISAMHGERRLKPKCGPAAITDRNDIGSSRSSSSAMSSSSAS		60
hb	1	MSLSFLLLPFSSHILISAMHGERRLKPKCGPAAITDRNDIGSSRSSSSAMSSSSAS		60

QY 1 MSLSFLLLLFTSHLILSAMAHGKRLAKPGQPGPATDTRNPICGSSSRQSSSAMSSSSAS 600

Db 1 MSLSFLLLLFTSHLILSAMAHGKRLAKPGQPGPATDTRNPICGSSSRQSSSAMSSSSAS 600

QY 61 SSPASISGSGSGLBOSSPQSGRRGSLYCRVIGIHLQIYPDGVNGSHEANMLSV 120
DB 61 SSPASISGSGSGLBOSSPQSGRRGSLYCRVIGIHLQIYPDGVNGSHEANMLSV 120
QY 121 LEIFAVSOGIVGIRGVFSNKFPLAMSKKGLHASAKFTDDCKRFRFOENSNTYVYASAIHR 180
DB 121 LEIFAVSOGIVGIRGVFSNKFPLAMSKKGLHASAKFTDDCKRFRFOENSNTYVYASAIHR 180
QY 181 TEKTRGEMVVALNKGKAKRGCSPRVYKPOHISTHFLPRFKOSBOPELSTFTVTPPEKNPP 240
DB 181 TEKTRGEMVVALNKGKAKRGCSPRVYKPOHISTHFLPRFKOSBOPELSTFTVTPPEKNPP 240
QY 241 SPIKSKIPISAPRKNTNSVYKRLKFRFG 268
DB 241 SPIKSKIPISAPRKNTNSVYKRLKFRFG 268

RESULT 11

US-09-390-207-20
Sequence 20, Application US/09390207
Patent No. 6504530
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-09-390-207-20

Query Match 100.0%; Score 268; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.6e-244; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLLFPSHLILISAWAHGKRLAPKQGPAPATDNRNPIGSSRSOSSSAMSSSSAS 60
DB 1 MSLSFLLLFPSHLILISAWAHGKRLAPKQGPAPATDNRNPIGSSRSOSSSAMSSSSAS 60
QY 61 SSPASISGSGSGLBOSSPQSGRRGSLYCRVIGIHLQIYPDGVNGSHEANMLSV 120
DB 61 SSPASISGSGSGLBOSSPQSGRRGSLYCRVIGIHLQIYPDGVNGSHEANMLSV 120
QY 121 LEIFAVSOGIVGIRGVFSNKFPLAMSKKGLHASAKFTDDCKRFRFOENSNTYVYASAIHR 180
DB 121 LEIFAVSOGIVGIRGVFSNKFPLAMSKKGLHASAKFTDDCKRFRFOENSNTYVYASAIHR 180
QY 181 TEKTRGEMVVALNKGKAKRGCSPRVYKPOHISTHFLPRFKOSBOPELSTFTVTPPEKNPP 240
DB 181 TEKTRGEMVVALNKGKAKRGCSPRVYKPOHISTHFLPRFKOSBOPELSTFTVTPPEKNPP 240
QY 241 SPIKSKIPISAPRKNTNSVYKRLKFRFG 268
DB 241 SPIKSKIPISAPRKNTNSVYKRLKFRFG 268

RESULT 12

US-09-229-947-33
Sequence 33, Application US/09229947
Patent No. 6518236
GENERAL INFORMATION:
APPLICANT: Deisher, Theresa A.
APPLICANT: Conklin, Darrell C.
APPLICANT: Raymond, Fenella
APPLICANT: Bukowski, Thomas R.
APPLICANT: Holdeman, Susan D.
APPLICANT: Hansen, Birgit

APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFERENCE: 96-2001
CURRENT APPLICATION NUMBER: US/09/229,947
CURRENT FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FaetsEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-09-229-947-33

Query Match 100.0%; Score 268; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.6e-244; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFPSHLILISAWAHGKRLAPKQGPAPATDNRNPIGSSRSOSSSAMSSSSAS 60
DB 1 MSLSFLLLFPSHLILISAWAHGKRLAPKQGPAPATDNRNPIGSSRSOSSSAMSSSSAS 60
QY 61 SSPASISGSGSGLBOSSPQSGRRGSLYCRVIGIHLQIYPDGVNGSHEANMLSV 120
DB 61 SSPASISGSGSGLBOSSPQSGRRGSLYCRVIGIHLQIYPDGVNGSHEANMLSV 120
QY 121 LEIFAVSOGIVGIRGVFSNKFPLAMSKKGLHASAKFTDDCKRFRFOENSNTYVYASAIHR 180
DB 121 LEIFAVSOGIVGIRGVFSNKFPLAMSKKGLHASAKFTDDCKRFRFOENSNTYVYASAIHR 180
QY 181 TEKTRGEMVVALNKGKAKRGCSPRVYKPOHISTHFLPRFKOSBOPELSTFTVTPPEKNPP 240
DB 181 TEKTRGEMVVALNKGKAKRGCSPRVYKPOHISTHFLPRFKOSBOPELSTFTVTPPEKNPP 240
QY 241 SPIKSKIPISAPRKNTNSVYKRLKFRFG 268
DB 241 SPIKSKIPISAPRKNTNSVYKRLKFRFG 268

RESULT 13

US-09-572-406B-11
Sequence 11, Application US/09572406B
Patent No. 6605441
GENERAL INFORMATION:
APPLICANT: Alderson, Ralph et al.
TITLE OF INVENTION: Fibroblast Growth Factor 11
FILE REFERENCE: PFI84P1
CURRENT APPLICATION NUMBER: US/09/572,406B
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60/135,524
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 09/514,587
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 09/093,585
PRIOR FILING DATE: 1998-06-08
PRIOR APPLICATION NUMBER: 08/464,590
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-09-572-406B-11

Query Match 100.0%; Score 268; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.6e-244; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFPSHLILISAWAHGKRLAPKQGPAPATDNRNPIGSSRSOSSSAMSSSSAS 60
DB 1 MSLSFLLLFPSHLILISAWAHGKRLAPKQGPAPATDNRNPIGSSRSOSSSAMSSSSAS 60
QY 61 SSPASISGSGSGLBOSSPQSGRRGSLYCRVIGIHLQIYPDGVNGSHEANMLSV 120

Db 61 SSPASISGSGGLEGGSFQWSPSGRRTSGLYCRVIGIHLQIYPDGKXNGSHENMLSV 120
Qy 121 LEIPAVSGIIVGIRGVSNKFLAMSKGGLHSAKFTDDCKRERFQENSYNTYASAIHR 180
Db 121 LEIPAVSGIIVGIRGVSNKFLAMSKGGLHSAKFTDDCKRERFQENSYNTYASAIHR 180
Qy 181 TEKTRERWVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEOPELSTFTVVPKKNP 240
Db 181 TEKTRERWVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEOPELSTFTVVPKKNP 240
Qy 241 SPIKSIPLSAPRKNTNSVKYRLKFRFG 268
Db 241 SPIKSIPLSAPRKNTNSVKYRLKFRFG 268
RESULT 14
US-09-240-952-5
; Sequence 5, Application US/09240952
; Patent No. 631523
; GENERAL INFORMATION:
; APPLICANT: Kijavir, Ivar
; APPLICANT: La Fleur, Monique
; TITLE OF INVENTION: Method of Preventing the Death of Retinal
; TITLE OF INVENTION: Neurons and Treating Ocular Diseases
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,952
; FILING DATE: 29-Jan-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/041,383
; FILING DATE: 12-Mar-98
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1088P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
US-09-240-952-5
Query Match 84.3%; Score 226; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 RERFQENSYNTYASAIHRTEKTRERWVALNKGKAKRGCSPRVKPOHISTHFLPRFKOS 201
Qy 223 RERFQENSYNTYASAIHRTEKTRERWVALNKGKAKRGCSPRVKPOHISTHFLPRFKOS 268
Db 202 RERFQENSYNTYASAIHRTEKTRERWVALNKGKAKRGCSPRVKPOHISTHFLPRFKOS 247
RESULT 15
US-09-240-952-3
; Sequence 3, Application US/09240952
; Patent No. 631523
; GENERAL INFORMATION:
; APPLICANT: Kijavir, Ivar
; APPLICANT: La Fleur, Monique
; TITLE OF INVENTION: Method of Preventing the Death of Retinal
; TITLE OF INVENTION: Neurons and Treating Ocular Diseases
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,952
; FILING DATE: 29-Jan-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/041,383
; FILING DATE: 12-Mar-98
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1088P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-240-952-3
Query Match 84.3%; Score 226; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 11, 2006, 03:43:02
Job time : 21 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 03:43:56 ; Search time 9.5 Seconds
(without alignments)
879.942 Million cell updates/sec

Title: US-10-089-485-4

Perfect score: 268
Sequence: 1 MSLSFLLLPFSHILISAMA.....LSAPRXNTNSVXNRKPRFG 268

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 184161 seqs, 31191982 residues

Word size : 1

Total number of hits satisfying chosen parameters: 184041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 5: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 6: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 7: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	100.0	268	7	US-11-134-703-4
2	246	91.8	246	7	US-11-134-703-10
3	195	72.8	246	7	US-11-134-703-12
4	195	72.8	268	7	US-11-134-703-18
5	182	67.9	266	7	US-11-238-936-15
6	176	65.7	176	7	US-11-134-703-6
7	151	56.3	266	7	US-11-238-936-9
8	145	54.1	176	7	US-11-134-703-8
9	60	22.4	60	7	US-11-134-703-19
10	52	19.4	52	7	US-11-134-703-37
11	49	18.3	49	7	US-11-134-703-38
12	48	17.9	48	7	US-11-134-703-36
13	10	3.7	10	7	US-11-134-703-32
14	9	3.4	188	7	US-11-087-099-8568
15	9	3.4	413	7	US-11-096-568A-20771
16	9	3.4	446	6	US-10-714-887-214
17	8	3.0	10	7	US-11-134-703-33
18	8	3.0	153	7	US-11-096-568A-5443
19	8	3.0	202	6	US-10-793-626-1108
20	8	3.0	205	7	US-11-238-936-8
21	8	3.0	207	7	US-11-238-936-10
22	8	3.0	333	7	US-11-096-568A-26084
23	8	3.0	384	7	US-11-096-568A-33509
24	8	3.0	388	7	US-11-096-568A-33508
25	8	3.0	396	7	US-11-096-568A-33507

26	8	3.0	791	6	US-10-821-234-962	Sequence 962, App
27	8	3.0	3969	6	US-10-974-127A-59	Sequence 59, Appl
28	7	2.6	25	7	US-11-058-735-61	Sequence 61, Appl
29	7	2.6	54	7	US-11-150-054A-34	Sequence 34, Appl
30	7	2.6	98	6	US-10-510-386-138	Sequence 138, App
31	7	2.6	110	7	US-11-072-512-3422	Sequence 3422, App
32	7	2.6	112	7	US-11-096-568A-7612	Sequence 7612, Ap
33	7	2.6	115	7	US-11-004-399-2629	Sequence 2629, Ap
34	7	2.6	133	6	US-10-523-362-22	Sequence 22, Appl
35	7	2.6	141	7	US-11-096-568A-13393	Sequence 13393, A
36	7	2.6	163	7	US-11-172-740-2378	Sequence 2378, Ap
37	7	2.6	164	7	US-11-207-847-4	Sequence 4, Appl1
38	7	2.6	176	7	US-11-096-568A-7838	Sequence 7838, Ap
39	7	2.6	180	7	US-11-096-568A-12758	Sequence 12758, A
40	7	2.6	186	7	US-11-044-889-21	Sequence 21, Appl
41	7	2.6	186	7	US-11-044-889-22	Sequence 22, Appl
42	7	2.6	186	7	US-11-096-568A-17455	Sequence 17455, A
43	7	2.6	191	6	US-10-991-285-873	Sequence 873, App
44	7	2.6	193	7	US-11-238-936-11	Sequence 11, Appl
45	7	2.6	198	7	US-11-096-568A-18593	Sequence 18593, A

ALIGNMENTS

RESULT 1
US-11-134-703-4
; Sequence 4, Application US/11134703
; Publication No. US20060009393A1
; GENERAL INFORMATION:
; APPLICANT: Handa et al.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/11/134, 703
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427, 920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089, 485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 4
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-703-4

Query Match 100.0%; Score 268; DB 7; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.2e-247; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLPFSHILISAMAGKRLAPKQPGPAATDRNDIGSSSRGSSAMSSSAS 60
DB 1 MSLSFLLLPFSHILISAMAGKRLAPKQPGPAATDRNDIGSSSRGSSAMSSSAS 60
QY 61 SSPAASLQSSGSLFQSSFGWSPGRRGSLYCRVIGIFHLQIYDPGKVNNSHEANMLSV 120
DB 61 SSPAASLQSSGSLFQSSFGWSPGRRGSLYCRVIGIFHLQIYDPGKVNNSHEANMLSV 120
QY 121 LEIPAVSGIYIGIVGSPFNKFLAMSKKGKLAFAKFTDDCKFRFRPOENSNTYASAIHR 180
DB 121 LEIPAVSGIYIGIVGSPFNKFLAMSKKGKLAFAKFTDDCKFRFRPOENSNTYASAIHR 180
QY 181 TEKGRREYVALNTRGAKRKCSPRVKPHISTHFLPFRKQSBQPELSFTYVPEKKNP 240
DB 181 TEKGRREYVALNTRGAKRKCSPRVKPHISTHFLPFRKQSBQPELSFTYVPEKKNP 240

QY 163 RRPFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRYKPOHISTHFLPRFKOS 222
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Db 163 RRPFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRYKPOHISTHFLPRFKOS 222
| | | | |
QY 223 RRPFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRYKPOHISTHFLPRFKOS 237
| | | | |
Db 223 RRPFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRYKPOHISTHFLPRFKOS 237
| | | | |

RESULT 5
US-11-238-936-15
; Sequence 15, Application US/11238936
; Publication No. US20060025343A1
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha J.
; TITLE OF INVENTION: Angiogenesisally Effective Unit Dose of FGF and Method of
; FILE REFERENCE: 1296/12169S05
; CURRENT APPLICATION NUMBER: US/11/238, 936
; PRIOR FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: US/09/417, 721
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/104,103
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 15
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human FGF-5
US-11-238-936-15

Query Match 67.9%; Score 182; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 RTGSLYCRVIGIGFHLQIYDPDKVNGSHEANMLSVLEIFAVSQGIVGIRGVSNKFLAMSK 146
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Db 85 RTGSLYCRVIGIGFHLQIYDPDKVNGSHEANMLSVLEIFAVSQGIVGIRGVSNKFLAMSK 144
| | | | |
QY 147 KGKHAASAKFTDDCKFRFRFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRY 206
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Db 145 KGKHAASAKFTDDCKFRFRFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRY 204
| | | | |
QY 207 KPOHISTHFLPRFKOSEPBLSTFTVTPPEKKNPSPISKIPLSAPRKNTNSVYKRLKFR 266
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Db 205 KPOHISTHFLPRFKOSEPBLSTFTVTPPEKKNPSPISKIPLSAPRKNTNSVYKRLKFR 264
| | | | |
QY 267 FG 268
| | | | |
Db 265 FG 266
| | | | |

RESULT 6
US-11-134-703-6
; Sequence 6, Application US/1134703
; Publication No. US20060009393A1
; GENERAL INFORMATION:
; APPLICANT: Hanada et al.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT APPLICATION NUMBER: US/11/134, 703
; PRIOR FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427, 920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089, 485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent Ver. 3.3
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-703-6

Query Match 65.7%; Score 176; DB 7; Length 176;
Best Local Similarity 100.0%; Pred. No. 6.7e-160;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CRVIGIGFHLQIYDPDKVNGSHEANMLSVLEIFAVSQGIVGIRGVSNKFLAMSKGKHA 152
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Db 1 CRVIGIGFHLQIYDPDKVNGSHEANMLSVLEIFAVSQGIVGIRGVSNKFLAMSKGKHA 60
| | | | |
QY 153 SAKFTDDCKFRFRFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRYKPOHIS 212
| | | | |
Db 61 SAKFTDDCKFRFRFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRYKPOHIS 120
| | | | |
QY 213 THFLPRFKOSEPBLSTFTVTPPEKKNPSPISKIPLSAPRKNTNSVYKRLKFRFG 268
| | | | |
Db 121 THFLPRFKOSEPBLSTFTVTPPEKKNPSPISKIPLSAPRKNTNSVYKRLKFRFG 176
| | | | |

RESULT 7
US-11-238-936-9
; Sequence 9, Application US/11238936
; Publication No. US20060025343A1
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha J.
; TITLE OF INVENTION: Angiogenesisally Effective Unit Dose of FGF and Method of
; FILE REFERENCE: 1296/12169S05
; CURRENT APPLICATION NUMBER: US/11/238, 936
; PRIOR FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: US/09/417, 721
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/104,103
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 9
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human FGF-5
US-11-238-936-9

Query Match 56.3%; Score 151; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.8e-136;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 RTGSLYCRVIGIGFHLQIYDPDKVNGSHEANMLSVLEIFAVSQGIVGIRGVSNKFLAMSK 146
| | | | |
Db 85 RTGSLYCRVIGIGFHLQIYDPDKVNGSHEANMLSVLEIFAVSQGIVGIRGVSNKFLAMSK 144
| | | | |
QY 147 KGKHAASAKFTDDCKFRFRFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRY 206
| | | | |
Db 145 KGKHAASAKFTDDCKFRFRFOENSYNTYASAIHRTKTKGREWYVALNKRKAGCSPRY 204
| | | | |
QY 207 KPOHISTHFLPRFKOSEPBLSTFTVTPPEKKNPSPISKIPLSAPRKNTNSVYKRLKFR 266
| | | | |
Db 205 KPOHISTHFLPRFKOSEPBLSTFTVTPPEKKNPSPISKIPLSAPRKNTNSVYKRLKFR 264
| | | | |

RESULT 8
US-11-134-703-8
; Sequence 8, Application US/1134703
; Publication No. US20060009393A1
; GENERAL INFORMATION:

```
APPLICANT: Hanada et al.
TITLE OF INVENTION: IMMUNOGENIC EPTIOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
FILE REFERENCE: 67015-05
CURRENT APPLICATION NUMBER: US/11/134,703
CURRENT FILING DATE: 2005-05-19
PRIOR APPLICATION NUMBER: PCT/US2003/37065
PRIOR FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US 60/427,920
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 10/089,485
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26689
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/157,103
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 8
LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
US-11-134-703-8

Query Match          54.1% Score 145; DB 7; Length 176;
Best Local Similarity 100.0%; Pred. No. 2e-130;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CRVGIGFHLQIYPDGKNGSHANMLSVLEIPAVSGQIGVINGVSNKFLAMSKGKLA 152
DB 1 CRVGIGFHLQIYPDGKNGSHANMLSVLEIPAVSGQIGVINGVSNKFLAMSKGKLA 60
QY 153 SAKFTDDCKFRFRFQENSNTYASAIHRTKRGREMYVALNKGKAKGCGSPRVKPOHIS 212
DB 61 SAKFTDDCKFRFRFQENSNTYASAIHRTKRGREMYVALNKGKAKGCGSPRVKPOHIS 120
QY 213 THFLPRFQSEQPELSFTYVPEKK 237
DB 121 THFLPRFQSEQPELSFTYVPEKK 145

RESULT 9
US-11-134-703-19
; Sequence 19, Application US/11134703
; Publication No. US2006000933A1
; GENERAL INFORMATION:
; APPLICANT: Hanada et al.
; TITLE OF INVENTION: IMMUNOGENIC EPTIOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT APPLICATION NUMBER: US/11/134,703
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427,920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089,485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-703-19

Query Match          22.4% Score 60; DB 7; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.1e-50;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 KFRERFQENSNTYASAIHRTKRGREMYVALNKGKAKGCGSPRVKPOHIS 220
```

```
DB 1 KFRERFQENSNTYASAIHRTKRGREMYVALNKGKAKGCGSPRVKPOHIS 60

RESULT 10
US-11-134-703-37
; Sequence 37, Application US/11134703
; Publication No. US2006000933A1
; GENERAL INFORMATION:
; APPLICANT: Hanada et al.
; TITLE OF INVENTION: IMMUNOGENIC EPTIOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT APPLICATION NUMBER: US/11/134,703
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427,920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089,485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 37
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant peptide sequence.
US-11-134-703-37

Query Match          19.4% Score 52; DB 7; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.8e-42;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 KFRERFQENSNTYASAIHRTKRGREMYVALNKGKAKGCGSPRVKPOHIS 212
DB 1 KFRERFQENSNTYASAIHRTKRGREMYVALNKGKAKGCGSPRVKPOHIS 52

RESULT 11
US-11-134-703-38
; Sequence 38, Application US/11134703
; Publication No. US2006000933A1
; GENERAL INFORMATION:
; APPLICANT: Hanada et al.
; TITLE OF INVENTION: IMMUNOGENIC EPTIOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT APPLICATION NUMBER: US/11/134,703
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427,920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089,485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 38
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant peptide sequence.
US-11-134-703-38
```


Query Match 18.3%; Score 49; DB 7; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 NTYASAIHRTKRGREYVALNKRGRKAGCSPRVKPOHISTHFLPRFX 220
Db 1 NTYASAIHRTKRGREYVALNKRGRKAGCSPRVKPOHISTHFLPRFX 49

RESULT 12
US-11-134-703-36

Sequence 36, Application US/11134703
Publication No. US20060009393A1
GENERAL INFORMATION:

APPLICANT: Hanada et al.

TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)

FILE REFERENCE: 67015-05

CURRENT FILING DATE: 2005-05-19

PRIOR APPLICATION NUMBER: PCT/US2003/37065

PRIOR FILING DATE: 2003-11-19

PRIOR APPLICATION NUMBER: US 60/427,920

PRIOR FILING DATE: 2002-11-19

PRIOR APPLICATION NUMBER: US 10/089,485

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26689

PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: 60/157,103

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 3.3

SEQ ID NO 36

LENGTH: 48

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Variant peptide sequence.

US-11-134-703-36

Query Match 17.9%; Score 48; DB 7; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.1e-38;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 TYASAIHRTKRGREYVALNKRGRKAGCSPRVKPOHISTHFLPRFX 220
Db 1 TYASAIHRTKRGREYVALNKRGRKAGCSPRVKPOHISTHFLPRFX 48

RESULT 13
US-11-134-703-32

Sequence 32, Application US/11134703
Publication No. US20060009393A1
GENERAL INFORMATION:

APPLICANT: Hanada et al.

TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)

FILE REFERENCE: 67015-05

CURRENT FILING DATE: 2005-05-19

PRIOR APPLICATION NUMBER: PCT/US2003/37065

PRIOR FILING DATE: 2003-11-19

PRIOR APPLICATION NUMBER: US 60/427,920

PRIOR FILING DATE: 2002-11-19

PRIOR APPLICATION NUMBER: US 10/089,485

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26689

PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: 60/157,103

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 3.3

SEQ ID NO 32

LENGTH: 10

TYPE: PRT

ORGANISM: homo sapiens
US-11-134-703-32

Query Match 3.7%; Score 10; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 MLSTVLEIFAV 126
Db 1 MLSTVLEIFAV 10

RESULT 14
US-11-087-099-8568

Sequence 8568, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53450)B-EP

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 8568

LENGTH: 188

TYPE: PRT

ORGANISM: Sorghum bicolor

US-11-087-099-8568

Query Match 3.4%; Score 9; DB 7; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 SASSSPAS 66
Db 114 SASSSPAS 122

RESULT 15
US-11-096-568A-20771

Sequence 20771, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nikolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

FILE REFERENCE: 2750-1592PUS2

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 20771

LENGTH: 413

TYPE: PRT

ORGANISM: Zea mays subsp. mays

FEATURE: NAME/KEY: misc.feature

LOCATION: (1)-(413)

OTHER INFORMATION: Ceres Seq. ID no. 12387083

US-11-096-568A-20771

Query Match 3.4%; Score 9; DB 7; Length 413;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 SSSSASSSP 63
Db 243 SSSSASSSP 251

Search completed: April 11, 2006, 03:46:10
Job time : 9.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 03:36:56 ; Search time 13 Seconds
(without alignments)
1983.546 Million cell updates/sec

Title: US-10-089-485-4

Perfect score: 268

Sequence: 1 MSLSFLLLPFSHLILSAMA.....LSAPRKNTNSVKYRLKRFPG 268

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: p1r1:*
- 2: p1r2:*
- 3: p1r3:*
- 4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182	67.9	267	1	TVHUP5
2	90	33.6	264	2	A36207
3	90	33.6	266	2	S68144
4	39	14.6	121	2	S68145
5	10	3.7	109	2	S68307
6	9	3.4	143	2	T22906
7	9	3.4	979	2	T01566
8	8	3.0	153	2	S67294
9	8	3.0	202	1	TVMSHS
10	8	3.0	206	1	TVHUS
11	8	3.0	206	2	JCA268
12	8	3.0	208	2	S20102
13	8	3.0	208	2	S14192
14	8	3.0	225	2	B84653
15	8	3.0	229	2	JC7219
16	8	3.0	238	2	S77699
17	8	3.0	238	2	D84585
18	8	3.0	262	2	T40941
19	8	3.0	264	2	D96694
20	8	3.0	268	2	C84585
21	8	3.0	270	2	F86170
22	8	3.0	299	2	T52452
23	8	3.0	325	2	H96815
24	8	3.0	354	2	S39406
25	8	3.0	391	2	S61704
26	8	3.0	396	2	T26987
27	8	3.0	412	2	S30299
28	8	3.0	419	2	T49292
29	8	3.0	429	2	A47305

30	8	3.0	431	2	T12450	hypothetical prote
31	8	3.0	459	2	A68712	protein C17H12.9 l
32	8	3.0	472	2	T04699	hypothetical prote
33	8	3.0	484	2	S66713	hypothetical prote
34	8	3.0	490	2	A32140	steroid 15beta-mon
35	8	3.0	559	1	RWBYS1	glycophospholipid-
36	8	3.0	600	2	S07638	spore coat protein
37	8	3.0	640	1	OQBEU2	U135 protein - hum
38	8	3.0	640	2	S62747	homeotic protein A
39	8	3.0	661	2	T16597	hypothetical prote
40	8	3.0	717	2	T25431	hypothetical prote
41	8	3.0	741	2	I48694	probable transcrip
42	8	3.0	742	2	A49672	transcription fact
43	8	3.0	772	2	A55004	transcription fact
44	8	3.0	775	1	EDBE11	transcription fact
45	8	3.0	825	1	EDBE11	transcription fact

ALIGNMENTS

RESULT 1

TVHUP5
fibroblast growth factor 5 - human
N:Alternate names: transforming protein FGFS
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A31194
R:Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Mol. Cell. Biol. 8, 3487-3495, 1988
A>Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth f
A:Reference number: A31194, MUID:89096942, PMID:3211147
A:Accession: A31194
A:Molecule type: mRNA
A:Residues: 1-267 <ZHA>
A:Cross-references: UNIPROT:P12034; UNIPARC:UPI00000462BB; GB:M23536; GB:M21617; NID:G14
C:Genetics:
A:Gene: GDB:FGFS
A:Cross-references: GDB:119907; OMIM:165190
A:Map position: 4q21-4q21
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match 67.9%; Score 182; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.6e-169;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	87	RTGSLYCRVGI	GFHLQIY	PDGKNGS	HEANMLSVLEIF	FAVSGT	VGIRGV	SNKFL	AMSK	146
DB	86	RTGSLYCRVGI	GFHLQIY	PDGKNGS	HEANMLSVLEIF	FAVSGT	VGIRGV	SNKFL	AMSK	145
QY	147	KGKLHSAKFT	DDCKFRER	FOENSNT	YASAIHRT	TEKGR	EMVVALN	RGR	AKGCS	PRV 206
DB	146	KGKLHSAKFT	DDCKFRER	FOENSNT	YASAIHRT	TEKGR	EMVVALN	RGR	AKGCS	PRV 205
QY	207	KPOHISTH	FLPRFKQ	SEOP	ELSFY	TVDEK	KNPPSP	PIKSK	PLS	APRKNTNSVKYRLKRF 266
DB	206	KPOHISTH	FLPRFKQ	SEOP	ELSFY	TVDEK	KNPPSP	PIKSK	PLS	APRKNTNSVKYRLKRF 265
QY	267	FG	268							
DB	266	FG	267							

RESULT 2

A36207
fibroblast growth factor 5 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: A36207; B37360
R:Hand, O.; Drucker, B.; Goldfarb, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 8022-8026, 1990
A>Title: Expression of the murine fibroblast growth factor 5 gene in the adult central n

A:Reference number: A36207; MUID:91045929; PMID:1700424
A:Accession: A36207
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-264 <HAU>
A:Cross-references: UNIPROT:P15656; UNIPARC:UPI000003F7B; GB:M37821; GB:M37822; GB:M37823
R:Hebert, J.M.; Basillio, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A:Reference number: A37360; MUID:90201563; PMID:2318343
A:Accession: B37360
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <HEB>
A:Cross-references: UNIPARC:UPI000003F7B; GB:M30643; NID:9193294; PTDN:AAA96698.1; PID:
C:Superfamily: fibroblast growth factor

Query Match 33.6%; Score 90; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 8.8e-80; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 LEIFAVSOGIVGIRGVSNKFLAMSKKGLTASAKFTDDCKFRERFOENSYNTTASAIHR 180
|||
119 LEIFAVSOGIVGIRGVSNKFLAMSKKGLTASAKFTDDCKFRERFOENSYNTTASAIHR 178
|||

Qy 181 TEXTGREWYVALNKRKGAKRGCSPPVAKPOH 210
|||
179 TEXTGREWYVALNKRKGAKRGCSPPVAKPOH 208
|||

RESULT 3
S68144
fibroblast growth factor 5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68144
R:Hatton, Y.; Yamasaki, M.; Itoh, N.
Biochim. Biophys. Acta 1306, 31-33, 1996
A:Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel tr
A:Reference number: S68144; MUID:96201703; PMID:8611621
A:Accession: S68144
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-266 <HAT>
A:Cross-references: UNIPROT:P48807; UNIPARC:UPI000012A716; EMBL:D64085; NID:992952; PID:
C:Superfamily: fibroblast growth factor

Query Match 33.6%; Score 90; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 8.8e-80; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 LEIFAVSOGIVGIRGVSNKFLAMSKKGLTASAKFTDDCKFRERFOENSYNTTASAIHR 180
|||
119 LEIFAVSOGIVGIRGVSNKFLAMSKKGLTASAKFTDDCKFRERFOENSYNTTASAIHR 178
|||

Qy 181 TEXTGREWYVALNKRKGAKRGCSPPVAKPOH 210
|||
179 TEXTGREWYVALNKRKGAKRGCSPPVAKPOH 208
|||

RESULT 4
S68145
fibroblast growth factor 5, truncated splice form - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68145
R:Hatton, Y.; Yamasaki, M.; Itoh, N.
Biochim. Biophys. Acta 1306, 31-33, 1996
A:Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel tr
A:Reference number: S68144; MUID:96201703; PMID:8611621
A:Accession: S68145
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA

```

A:Residues: 1-121 <HAT>
A:Cross-references: UNIPROT:P48607; UNIPARC:UP100000298F; EMBL:D64086; NID:g987689; PID
C:Keywords: alternative splicing

Query Match          14.6%; Score 39; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2,6e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 SFFQWSPGSRRTGSLYCRVIGICFHLQIYDPGKNGSHEA 115
      |||||
DB 75 SFFQWSPGSRRTGSLYCRVIGICFHLQIYDPGKNGSHEA 113

RESULT 5
S69307
probable membrane protein YLR294c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L8003.19-a
C:Species: Saccharomyces cerevisiae
C:Date: 20-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: S69307
R:Pauley, A.
submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid 8003.
A:Reference number: S50366
A:Accession: S69307
A:Molecule type: DNA
A:Residues: 1-109 <PAU>
A:Cross-references: UNIPROT:O13543; UNIPARC:UP1000004F949; EMBL:U17243; NID:g596030; PID
C:Genetic8:
A:Gene: MIPS:YLR294c
A:Cross-references: SGD:S0004285
A:Map position: 12R
C:Superfamily: Saccharomyces probable membrane protein YLR294c
C:Keywords: transmembrane protein
F:77-93/Domain: transmembrane #status predicted <TM>

Query Match          3.7%; Score 10; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLSFLLLF 11
      |||||
DB 82 SLSFLLLF 91

RESULT 6
T22906
hypothetical protein F58D12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22906
R:Percy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19635
A:Accession: T22906
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-143 <MIT>
A:Cross-references: UNIPROT:O02276; UNIPARC:UP100000753E8; EMBL:Z81092; PIDN:CAB03144.1,
A:Experimental source: clone F58D12
C:Genetic8:
A:Gene: CESP:F58D12.1
A:Map position: 5
A:Introns: 14/1, 36/2; 75/1; 90/3

Query Match          3.4%; Score 9; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SSSASSSPA 64
      |||||
DB 53 SSSASSSPA 61

```

```
RESULT 7
T01566
hypothetical protein A_TM018A10.23 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #ext_change 09-Jul-2004
C:Accession: T01566
R:Dempsey, S.; Harper, M.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of A. thaliana TM018A10.
A:Reference number: Z14348
A:Accession: T01566
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-979 <DEM>
A:Cross-references: UNIPROT:Q23096; UNIPARC:UPI000009EB61; EMBL:AF013294; NID:G2252848;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 466/3; 569/3; 649/3; 688/1; 740/3; 877/3
A>Note: A_TM018A10.23
C:Superfamily: Arabidopsis thaliana hypothetical protein A_TM018A10.23

Query Match      3.4%; Score 9; DB 2; Length 979;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 SSSASASSP 63
    |||||
    |||||
    |||||
Db 37 SSSASASSP 45

RESULT 8
S67294
hypothetical protein YOR382W - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O6760
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #ext_change 09-Jul-2004
A:Accession: S67294
R:Delius, H.; Hebling, U.; Hofmann, B.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67261
A:Accession: S67294
A:Molecule type: DNA
A:Residues: 1-153 <DEL>
A:Cross-references: UNIPROT:Q08906; UNIPARC:UPI000004F973; EMBL:Z75290; NID:G1420822; PI
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:FIT2; MIPS:YOR382W
A:Cross-references: SGD:S0005909
A:Map position: 15R

Query Match      3.0%; Score 8; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 SSSASASSS 62
    |||||
    |||||
    |||||
Db 122 SSSASASSS 129

RESULT 9
TWM5HS
fibroblast growth factor 4 - mouse
N:Alternate names: transforming protein hctf1; transforming protein k-FGF; transforming
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #ext_change 09-Jul-2004
A:Accession: S04741; A57360
R:Brooker, S.; Smith, R.; Thurlow, J.; Dickson, C.; Peters, G.
Nucleic Acids Res. 17, 4037-4045, 1989
A:Title: The mouse homologue of hst/k-FGF: sequence, genome organization and location re
A:Reference number: S04741; MUID:89296455; PMID:2740210
A:Accession: S04741
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```
A:Molecule type: DNA
A:Residues: 1-202 <BRO>
A:Cross-references: UNIPROT:P11403; UNIPARC:UPI0000027966; GB:X14849; GB:M28516; NID:952
R:Hebert, J.M.; Basilico, C.; Goldfarb, W.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A:Reference number: A37360; MUID:90201563; PMID:2318343
A:Accession: A37360
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166, 'S', 168-202 <HEB>
A:Cross-references: UNIPARC:UPI000000415D; GB:M30642; NID:G193290; PIDN:AAA37619.1; PID:
C:Genetics:
A:Gene: hst
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match      3.0%; Score 8; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 VGIGFHLQ 102
    |||||
    |||||
    |||||
Db 86 VGIGFHLQ 93

RESULT 10
TWM5HS
fibroblast growth factor 4 - human
N:Alternate names: heparin secretory transforming protein 1; Kaposi sarcoma oncogene; ti
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #ext_change 09-Jul-2004
A:Accession: A28417; A29876; A29649
R:Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Sug
Proc. Natl. Acad. Sci. U.S.A. 84, 7305-7309, 1987
A:Title: Genomic sequence of hst, a transforming gene encoding a protein homologous to f
A:Reference number: A28417; MUID:88041096; PMID:2959959
A:Accession: A28417
A:Molecule type: DNA
A:Residues: 1-206 <YOS>
A:Cross-references: UNIPROT:P08620; UNIPARC:UPI0000040662; DBJ:J02986; NID:G184430; PII
R:Taira, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A:Title: cDNA sequence of human transforming gene hst and identification of the coding s
A:Reference number: A29876; MUID:87204251; PMID:2953031
A:Accession: A29876
A:Molecule type: mRNA
A:Residues: 1-206 <TAI>
A:Cross-references: UNIPARC:UPI0000040662; GB:J02986; GB:M16338; NID:G184430; PIDN:AB55
R:Deilli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Iltmann, M.; Basilico, C.
Cell 50, 729-737, 1987
A:Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth f
A:Reference number: A29649; MUID:87301716; PMID:2957062
A:Accession: A29649
A:Molecule type: mRNA
A:Residues: 1-206 <BOV>
A:Cross-references: UNIPARC:UPI0000040662; GB:M17446; NID:G186785; PIDN:AAA59473.1; PID:
C:Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the mov
C:Genetics:
A:Gene: GDB:FGF4; HSTF1
A:Cross-references: GDB:120066; OMIM:164980
A:Map position: 11q13.3-11q13.3
A:Introns: 114/1; 148/3
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; Kaposi sarcoma; transforming protein

Query Match      3.0%; Score 8; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 VGIGFHLQ 102
    |||||
    |||||
    |||||
Db 90 VGIGFHLQ 97
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RESULT 11
JC4268
fibroblast growth factor 4 - bovine
N:Alternate names: transforming protein hst
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
C:Accession: J04268
R:Yu, J.C.; Desseabra, A.U.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Miki, T.; Heldaran,
Gene 162, 333-334, 1995
A:Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
A:Reference number: J04268; MUID:96032369; PMID:7557455
A:Accession: J04268
A:Molecule type: mRNA
A:Residues: 1-206 <YU>
A:Cross-references: UNIPARC:UPI0000176539; GB:U15969
A>Note: The authors translated the codon GGC for residue 114 as Ser
C:Comment: This protein is a member of fibroblast growth factor family. The hstgene in C
C:Genetics:
A:Gene: hst
A:Introns: 113/3; 145/2
C:Superfamily: fibroblast growth factor
C:Keywords: thymus; transforming protein

Query Match 3.0%; Score 8; DB 2; Length 206;
Best Local Similarity 100.0%; Pred.No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 VGIGFHLQ 102
|||||
DB 90 VGIGFHLQ 97

RESULT 12
S20102
fibroblast growth factor 6 precursor - human
N:Alternate names: fibroblast growth factor-related protein FGF.6; transforming protein
C:Species: Homo sapiens (man)
C:Date: 18-Feb-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: S20102; S23739; S04204; S36910
R:Coulter, F.; Batz, M.; Marica, I.; de Lapeyriere, O.; Birnbaum, D.
Oncogene 6, 1437-1444, 1991
A:Title: Putative structure of the FGF6 gene product and role of the signal peptide.
A:Reference number: S20102; MUID:91360279; PMID:1886714
A:Accession: S20102
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-208 <COU>
A:Cross-references: UNIPROT:P10767; UNIPARC:UPI00000411BF; EMBL:X57075
A>Note: It is uncertain whether Met-1 or Met-11 is the initiator
R:Ida, S.; Yoshida, T.; Naito, K.; Sakamoto, H.; Kato, O.; Hirohashi, S.; Sato, T.; On
Oncogene 7, 303-309, 1992
A:Title: Human hst-2 (FGF-6) oncogene: cDNA cloning and characterization.
A:Reference number: S23739; MUID:92195660; PMID:1549352
A:Accession: S23739
A:Molecule type: mRNA
A:Residues: 1-208 <ID>
A:Cross-references: UNIPARC:UPI00000411BF; EMBL:X63454
A>Note: It is uncertain whether Met-1 or Met-11 is the initiator
R:Marica, I.; Adelstein, J.; Raynaud, F.; Mattei, M.G.; Coulter, F.; Planche, J.; de Lape
Oncogene 4, 335-340, 1989
A:Title: Characterization of the HST-related FGF 6 gene, a new member of the fibroblast
A:Reference number: S04204; MUID:89201880; PMID:2649647
A:Accession: S04204
A:Molecule type: DNA
A:Residues: 81-99, 'G', 101-208 <MAR>
A:Cross-references: UNIPARC:UPI000016A8P6; EMBL:X14071; NID:G31354; PIDN:CA837648.2; PID
C:Genetics:
A:Gene: GDB:FGF6; hst-2
A:Cross-references: GDB:119908; OMIM:134921
A:Map position: 12p13-12p13
A:Introns: 115/3; 150/2

C:Superfamily: fibroblast growth factor
P:1-40/Domains: (or 11-40 or 34-40) signal sequence #status predicted <Sig>
F:41-208/Product: fibroblast growth factor 6 #status predicted <Mat>

Query Match 3.0%; Score 8; DB 2; Length 208;
Best Local Similarity 100.0%; Pred.No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 VGIGFHLQ 102
|||||
DB 92 VGIGFHLQ 99

RESULT 13
S14192
fibroblast growth factor 6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S14192; I49665; I49664
R:de Lapeyriere, O.; Rosnet, O.; Benharroch, D.; Raynaud, F.; Marchetto, S.; Planche, J.
Oncogene 5, 823-831, 1990
A:Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.
A:Reference number: S14192; MUID:90295275; PMID:2193291
A:Accession: S14192
A:Molecule type: DNA
A:Residues: 1-208 <LAP>
A:Cross-references: UNIPROT:P21658; UNIPARC:UPI000020A67; EMBL:X51552
A>Note: It is uncertain whether Met-1 or Met-11 is the initiator
R:Pollendorff, V.; Rosnet, O.; Marica, I.; Birnbaum, D.; deLapeyriere, O.
Biochimie 74, 1035-1038, 1992
A:Title: Isolation and sequence of the murine Fgf6 cDNA.
A:Reference number: I49664; MUID:93120244; PMID:1477139
A:Accession: I49665
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 19-208 <RES>
A:Cross-references: UNIPARC:UPI000016CD51; GB:M92416; NID:G193288; PIDN:AAA62261.1; PID
A:Accession: I49664
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RE2>
A:Cross-references: UNIPARC:UPI000016CD50; GB:M92415; NID:G193286; PIDN:AAA62260.1; PID
C:Genetics:
A:Gene: Fgf6
A:Introns: 116/1; 150/3
C:Superfamily: fibroblast growth factor

Query Match 3.0%; Score 8; DB 2; Length 208;
Best Local Similarity 100.0%; Pred.No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 VGIGFHLQ 102
|||||
DB 92 VGIGFHLQ 99

RESULT 14
B84653
TINY-like AP2 domain transcription factor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84653
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.B.; Umayam, L.; Tallon, L.
eues, D.; Niernan, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84653
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225 <STO>
A:Cross-references: UNIPROT:O82315; UNIPARC:UPI0000179899; GB:AE002093; NID:G3643601; PI

C:Genetics:
A:Gene: At2g25820
A:Map position: 2

Query Match
Best Local Similarity 3.0%; Score 8; DB 2; Length 225;
Matches 8; Conservative 100.0%; Pred. No. 7.4;
Mismatches 0; Indels 0; Gaps 0;

OY 55 SSSSASSS 62
|||
Db 140 SSSSASSS 147

RESULT 15

JC7219
nuclear protein SR-25 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: JC7219
R:Sasahara, K.; Yamaoka, T.; Moritani, M.; Tanaka, M.; Iwahana, H.; Yoshimoto, K.; Miyag
Biochem. Biophys. Res. Commun. 269, 444-450, 2000
A:Title: Molecular cloning and expression analysis of a putative nuclear protein, SR-25.
A:Reference number: JC7219; MUID:20175222; PMID:10708573
A:Accession: JC7219
A:Molecule type: mRNA
A:Residues: 1-229 <SAS-
A:Cross-references: UNIPROT:Q9JH93; UNIPARC:UPI00000231C4; DDBJ:AB035383; NID:G7619895;
A:Experimental source: M1N6 cell line
C:Comment: This protein is a highly hydrophilic nuclear protein with a serine-arginine r
A:splicing factors.
C:Keywords: nucleus; RNA processing

Query Match
Best Local Similarity 3.0%; Score 8; DB 2; Length 229;
Matches 8; Conservative 100.0%; Pred. No. 7.5;
Mismatches 0; Indels 0; Gaps 0;

OY 55 SSSSASSS 62
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Db 77 SSSSASSS 84

Search completed: April 11, 2006, 03:38:26
Job time : 13 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 03:43:16 ; Search time 60.5 Seconds
(without alignments)
1850.880 Million cell updates/sec

Title: US-10-089-485-4

Perfect score: 268
Sequence: 1 MSLSFLLLFSLHLSAWA.....LSAPRKTNSVKYRLKFRFG 268

Scoring table: OLIGO

Searched: 1867569 seqs, 417829326 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1866650

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

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4: /csm2_6/prodataa1/pubpaa/us10A_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	268	100.0	268	3	US-09-284-663A-10	Sequence 10, Appl
2	268	100.0	268	3	US-09-750-963-11	Sequence 11, Appl
3	268	100.0	268	3	US-09-902-773A-7	Sequence 7, Appl
4	268	100.0	268	3	US-09-251-763-12	Sequence 12, Appl
5	268	100.0	268	4	US-10-081-347-33	Sequence 33, Appl
6	268	100.0	268	4	US-10-169-960-14	Sequence 14, Appl
7	268	100.0	268	4	US-10-192-988-8	Sequence 8, Appl
8	268	100.0	268	4	US-10-315-431-33	Sequence 33, Appl
9	268	100.0	268	4	US-10-347-177-11	Sequence 11, Appl
10	268	100.0	268	4	US-10-372-653-11	Sequence 11, Appl
11	268	100.0	268	4	US-10-037-922-23	Sequence 23, Appl
12	268	100.0	268	5	US-10-854-485-33	Sequence 33, Appl
13	268	100.0	268	5	US-10-413-537-10	Sequence 10, Appl
14	268	84.3	268	3	US-09-345-373-15	Sequence 15, Appl
15	226	84.3	268	4	US-10-075-446-15	Sequence 15, Appl
16	226	84.3	268	4	US-10-035-212-15	Sequence 15, Appl
17	226	84.3	268	5	US-10-733-311-15	Sequence 15, Appl
18	226	84.3	268	5	US-10-668-577A-27	Sequence 27, Appl
19	226	84.3	268	5	US-10-901-310-15	Sequence 15, Appl
20	198	73.9	265	4	US-10-192-988-18	Sequence 18, Appl
21	182	67.9	247	4	US-10-023-592-9	Sequence 9, Appl
22	182	67.9	266	4	US-10-131-965-15	Sequence 15, Appl
23	182	67.9	267	3	US-09-832-485-8	Sequence 8, Appl
24	182	67.9	267	3	US-09-425-021-13	Sequence 13, Appl
25	182	67.9	267	4	US-10-023-592-7	Sequence 7, Appl
26	182	67.9	267	4	US-10-374-207-8	Sequence 8, Appl
27	182	67.9	267	4	US-10-123-481-7	Sequence 7, Appl

28	182	67	9	267	5	US-10-933-226-7	Sequence 7, Appl
29	182	67	9	267	5	US-10-933-224-7	Sequence 7, Appl
30	172	64	2	219	4	US-10-016-447-13	Sequence 13, Appl
31	151	56	3	266	4	US-10-123-965-9	Sequence 9, Appl
32	151	56	3	266	4	US-10-690-015-14	Sequence 14, Appl
33	144	53	7	144	3	US-09-901-938-27	Sequence 27, Appl
34	144	53	7	144	4	US-10-379-334-27	Sequence 27, Appl
35	51	19	0	82	3	US-09-801-968-39	Sequence 39, Appl
36	51	19	0	82	3	US-09-802-154-39	Sequence 39, Appl
37	11	4	1	173	4	US-10-767-701-61	Sequence 41, Appl
38	11	4	1	287	4	US-10-425-114-59971	Sequence 59971, A
39	10	3	7	10	3	US-09-572-4048-3798	Sequence 3798, Ap
40	10	3	7	10	3	US-09-572-4048-3799	Sequence 3799, Ap
41	10	3	7	109	4	US-10-457-467A-282	Sequence 282, App
42	10	3	7	359	4	US-10-437-963-187062	Sequence 187062, A
43	10	3	7	502	6	US-11-097-193-23466	Sequence 23466, A
44	9	3	4	9	4	US-10-424-955A-36	Sequence 36, Appl
45	9	3	4	9	5	US-10-982-514-37	Sequence 37, Appl

ALIGNMENTS

```

1 RESULT 1
2 US-09-284-663A-10
3 Sequence 10, Application US/09284663A
4 Patent No. US20020012961A1
5 GENERAL INFORMATION:
6 APPLICANT: Botstein, David A.
7 APPLICANT: Goddard, Audrey
8 APPLICANT: Gurney, Austin L.
9 APPLICANT: Hillan, Kenneth J.
10 APPLICANT: Lawrence, David A.
11 APPLICANT: Roy, Margaret Ann
12 TITLE OF INVENTION: Fibroblast Growth Factor-15
13 FILE REFERENCE: FI2191(e)
14 CURRENT APPLICATION NUMBER: US/09/284,663A
15 CURRENT FILING DATE: 1999-04-15
16 NUMBER OF SEQ ID NOS: 30
17 SEQ ID NO 10
18 LENGTH: 266
19 TYPE: FRT
20 ORGANISM: Homo sapiens
21 US-09-284-663A-10

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Query Match          100.0%; Score 268; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 4,3e-240;
Match 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1  MSLSFLLILFESHILISAMAHGKRLAPKGGPGPATATRNPIGSSRSSSSAMSSSSAS 60
DB      1  MSLSFLLILFESHILISAMAHGKRLAPKGGPGPATATRNPIGSSRSSSSAMSSSSAS 60

QY      61  SSPASISGSSGSGLEQSSFWSPSGRRTGSLYCRVGIQIYPDGKVNSGSHANMLSV 120
DB      61  SSPASISGSSGSGLEQSSFWSPSGRRTGSLYCRVGIQIYPDGKVNSGSHANMLSV 120

QY      121  LEIFAVSGIYGVINGVPSNKFLAMSKKGKLHASAKFTDDCKFRERFQENSYNTVASAIHR 180
DB      121  LEIFAVSGIYGVINGVPSNKFLAMSKKGKLHASAKFTDDCKFRERFQENSYNTVASAIHR 180

QY      181  TEXTGREYVALNTRGKAKRGCSPRVYKQIHSTHFLPFPKQSEQBELSFTVTPEKNPP 240
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QY      241  SPIKSKIPLSAPRKNTNSVYKTRLKPRRG 268
DB      241  SPIKSKIPLSAPRKNTNSVYKTRLKPRRG 268

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Patent No. US20020031805A1
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGP10
FILE REFERENCE: 99-83
CURRENT APPLICATION NUMBER: US/09/750,963
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,578
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 268
TYPE: PR1
ORGANISM: Homo sapiens
US-09-750-963-11

Query Match 100.0%; Score 268; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSLSFLLLFPSHLLISAWAHGKRLAPKGPAPATDNRNPIGSSSRSSGSSAMSSSAS 60
QY 61 SSPASISGSGSGLSQSSSFQWSPSGRRTGSLYCRVIGFHLQIYPDGKNGSHEANMLSV 120
DB 61 SSPASISGSGSGLSQSSSFQWSPSGRRTGSLYCRVIGFHLQIYPDGKNGSHEANMLSV 120
QY 121 LEIFAVSQIGVIRGVFNSKFLAMSKGKGLHASAKFTDDCKFRERFOENSNTYTSALHR 180
DB 121 LEIFAVSQIGVIRGVFNSKFLAMSKGKGLHASAKFTDDCKFRERFOENSNTYTSALHR 180
QY 181 TEKTRRWYVALNKGKAKRGCSPRVKPDHISTHFLPRFKOSEBQELSTVTVPEKKNP 240
DB 181 TEKTRRWYVALNKGKAKRGCSPRVKPDHISTHFLPRFKOSEBQELSTVTVPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 3
US-09-902-773A-7
Sequence 7, Application US/09902773A
Patent No. US20020034787A1

GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
GOCAYNE, JEANNINE D.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-10
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/902,773A
FILING DATE: 12-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,926
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0350001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-902-773A-7

Query Match 100.0%; Score 268; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFPSHLLISAWAHGKRLAPKGPAPATDNRNPIGSSSRSSGSSAMSSSAS 60
DB 1 MSLSFLLLFPSHLLISAWAHGKRLAPKGPAPATDNRNPIGSSSRSSGSSAMSSSAS 60
QY 61 SSPASISGSGSGLSQSSSFQWSPSGRRTGSLYCRVIGFHLQIYPDGKNGSHEANMLSV 120
DB 61 SSPASISGSGSGLSQSSSFQWSPSGRRTGSLYCRVIGFHLQIYPDGKNGSHEANMLSV 120
QY 121 LEIFAVSQIGVIRGVFNSKFLAMSKGKGLHASAKFTDDCKFRERFOENSNTYTSALHR 180
DB 121 LEIFAVSQIGVIRGVFNSKFLAMSKGKGLHASAKFTDDCKFRERFOENSNTYTSALHR 180
QY 181 TEKTRRWYVALNKGKAKRGCSPRVKPDHISTHFLPRFKOSEBQELSTVTVPEKKNP 240
DB 181 TEKTRRWYVALNKGKAKRGCSPRVKPDHISTHFLPRFKOSEBQELSTVTVPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 4
US-09-251-263-12
Sequence 12, Application US/09251263
Patent No. US20020052477A1

GENERAL INFORMATION:
APPLICANT: Nathan, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGUS
FILE REFERENCE: 07265/047003
CURRENT APPLICATION NUMBER: US/09/251,263
CURRENT FILING DATE: 1999-02-16
EARLIER APPLICATION NUMBER: 08/867,471
EARLIER FILING DATE: 1997-06-02
EARLIER APPLICATION NUMBER: 08/439,725
EARLIER FILING DATE: 1995-05-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 268
TYPE: PR1
ORGANISM: Homo sapiens
US-09-251-263-12

Query Match 100.0%; Score 268; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFPSHLLISAWAHGKRLAPKGPAPATDNRNPIGSSSRSSGSSAMSSSAS 60
DB 1 MSLSFLLLFPSHLLISAWAHGKRLAPKGPAPATDNRNPIGSSSRSSGSSAMSSSAS 60
QY 61 SSPASISGSGSGLSQSSSFQWSPSGRRTGSLYCRVIGFHLQIYPDGKNGSHEANMLSV 120

Db 61 SSPAASLGSQSGGLBQSSSFQWSPSGRRTGSLYCRVIGIHFHLQIYPDGKNGSHEANMLSV 120
QY 121 LEIFAVSGQIVGIRGVFNSKFLAMSKKGLHASAFPTDDCKRERFOENSNTYTSATHR 180
Db 121 LEIFAVSGQIVGIRGVFNSKFLAMSKKGLHASAFPTDDCKRERFOENSNTYTSATHR 180
QY 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEOPELSTVTVPEKKNP 240
Db 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEOPELSTVTVPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
Db 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 5
US-10-081-347-33
; Sequence 33, Application US/10081347
; Publication No. US20030008351A1
; GENERAL INFORMATION:
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Raymond, Penella
; APPLICANT: Bukowski, Thomas R.
; APPLICANT: Holderman, Susan D.
; APPLICANT: Hansen, Birgit
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
; FILE REFERENCE: 96-20C1
; CURRENT APPLICATION NUMBER: US/10/081,347
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US/09/229,947
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-347-33

Query Match 100.0%; Score 268; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLLFPSHLLISAMAHGEKRLAPKQGPAPATDNPIGSSRSROSSSAMSSSSAS 60
Db 1 MSLSFLLLFPSHLLISAMAHGEKRLAPKQGPAPATDNPIGSSRSROSSSAMSSSSAS 60
QY 61 SSPAASLGSQSGGLBQSSSFQWSPSGRRTGSLYCRVIGIHFHLQIYPDGKNGSHEANMLSV 120
Db 61 SSPAASLGSQSGGLBQSSSFQWSPSGRRTGSLYCRVIGIHFHLQIYPDGKNGSHEANMLSV 120
QY 121 LEIFAVSGQIVGIRGVFNSKFLAMSKKGLHASAFPTDDCKRERFOENSNTYTSATHR 180
Db 121 LEIFAVSGQIVGIRGVFNSKFLAMSKKGLHASAFPTDDCKRERFOENSNTYTSATHR 180
QY 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEOPELSTVTVPEKKNP 240
Db 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEOPELSTVTVPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
Db 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 6
US-10-189-360-14
; Sequence 14, Application US/10189360
; Publication No. US20030143217A1
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew

Chandler, Lois Ann
Sienowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESS: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/189,360
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030143217Aitenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= "FGF-5"
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-189-360-14

Query Match 100.0%; Score 268; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLLFPSHLLISAMAHGEKRLAPKQGPAPATDNPIGSSRSROSSSAMSSSSAS 60
Db 1 MSLSFLLLFPSHLLISAMAHGEKRLAPKQGPAPATDNPIGSSRSROSSSAMSSSSAS 60
QY 61 SSPAASLGSQSGGLBQSSSFQWSPSGRRTGSLYCRVIGIHFHLQIYPDGKNGSHEANMLSV 120
Db 61 SSPAASLGSQSGGLBQSSSFQWSPSGRRTGSLYCRVIGIHFHLQIYPDGKNGSHEANMLSV 120
QY 121 LEIFAVSGQIVGIRGVFNSKFLAMSKKGLHASAFPTDDCKRERFOENSNTYTSATHR 180
Db 121 LEIFAVSGQIVGIRGVFNSKFLAMSKKGLHASAFPTDDCKRERFOENSNTYTSATHR 180
QY 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEOPELSTVTVPEKKNP 240
Db 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEOPELSTVTVPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
Db 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 7
US-10-192-988-8
; Sequence 8, Application US/10192988
; Publication No. US20030166875A1
; GENERAL INFORMATION:

```
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: NATHANS, Jeremy
APPLICANT: SMALLWOOD, Philip M.
APPLICANT: MACKIE, Jennifer P.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR-2 AND METHODS OF USE
FILE REFERENCE: JHU1230-2
CURRENT APPLICATION NUMBER: US/10/192,988
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 09/261,007
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: US 08/438,439
PRIOR FILING DATE: 1995-05-12
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 268
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Mammalian
US-10-192-988-8
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Query Match      100.0%; Score 268; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MSLSTLLLFPSHLITLSAMAHGEKRLAPKGPAPATDRNPIGSSRSRQSSSAMSSSSAS 60
DB 1 MSLSTLLLFPSHLITLSAMAHGEKRLAPKGPAPATDRNPIGSSRSRQSSSAMSSSSAS 60
QY 61 SSPAASLGSQSGLEQSSFFQWSPSGRRTGSLYCRVIGIFHQLIYDPGKNGSHEANMLSV 120
DB 61 SSPAASLGSQSGLEQSSFFQWSPSGRRTGSLYCRVIGIFHQLIYDPGKNGSHEANMLSV 120
QY 121 LEIFAVSQGIVGIRGVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSYTTVSAIAHR 180
DB 121 LEIFAVSQGIVGIRGVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSYTTVSAIAHR 180
QY 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEBELSFTVTPPEKKNP 240
DB 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEBELSFTVTPPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
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```
RESULT 8
US-10-315-431-33
Sequence 33, Application US/10315431
Publication No. US20030199443A1
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```
GENERAL INFORMATION:
APPLICANT: Ellsworth, Jeff L.
APPLICANT: Delisher, Theresa A.
APPLICANT: Hughes, Steven D.
APPLICANT: Moore, Emma E.
APPLICANT: Wahl, Alan F.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFERENCE: 96-20C4
CURRENT APPLICATION NUMBER: US/10/315,431
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US/09/634,318
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-10-315-431-33
```

```
Query Match      100.0%; Score 268; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
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```
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSTLLLFPSHLITLSAMAHGEKRLAPKGPAPATDRNPIGSSRSRQSSSAMSSSSAS 60
DB 1 MSLSTLLLFPSHLITLSAMAHGEKRLAPKGPAPATDRNPIGSSRSRQSSSAMSSSSAS 60
QY 61 SSPAASLGSQSGLEQSSFFQWSPSGRRTGSLYCRVIGIFHQLIYDPGKNGSHEANMLSV 120
DB 61 SSPAASLGSQSGLEQSSFFQWSPSGRRTGSLYCRVIGIFHQLIYDPGKNGSHEANMLSV 120
QY 121 LEIFAVSQGIVGIRGVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSYTTVSAIAHR 180
DB 121 LEIFAVSQGIVGIRGVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSYTTVSAIAHR 180
QY 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEBELSFTVTPPEKKNP 240
DB 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEBELSFTVTPPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
```

```
RESULT 9
US-10-347-177-11
Sequence 11, Application US/10347177
Publication No. US20030220483A1
```

```
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Mackie, Jennifer P.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR-1 (FHF-1) AND METHODS
FILE REFERENCE: JHU1240-3
CURRENT APPLICATION NUMBER: US/10/347,177
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 09/251,263
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: US 08/867,471
PRIOR FILING DATE: 1997-06-02
PRIOR APPLICATION NUMBER: US 08/439,725
PRIOR FILING DATE: 1995-05-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-10-347-177-11
```

```
Query Match      100.0%; Score 268; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MSLSTLLLFPSHLITLSAMAHGEKRLAPKGPAPATDRNPIGSSRSRQSSSAMSSSSAS 60
DB 1 MSLSTLLLFPSHLITLSAMAHGEKRLAPKGPAPATDRNPIGSSRSRQSSSAMSSSSAS 60
QY 61 SSPAASLGSQSGLEQSSFFQWSPSGRRTGSLYCRVIGIFHQLIYDPGKNGSHEANMLSV 120
DB 61 SSPAASLGSQSGLEQSSFFQWSPSGRRTGSLYCRVIGIFHQLIYDPGKNGSHEANMLSV 120
QY 121 LEIFAVSQGIVGIRGVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSYTTVSAIAHR 180
DB 121 LEIFAVSQGIVGIRGVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSYTTVSAIAHR 180
QY 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEBELSFTVTPPEKKNP 240
DB 181 TEKTRREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEBELSFTVTPPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
```

```
RESULT 10
US-10-372-653-11
; Sequence 11, Application US/10372653
; Publication No. US20040048271A1
; GENERAL INFORMATION:
; APPLICANT: Alderson, Ralph et al.
; TITLE OF INVENTION: Fibroblast Growth Factor 11
; FILE REFERENCE: P184P1D1
; CURRENT APPLICATION NUMBER: US/10/372,653
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/572,406
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 60/135,524
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/514,587
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 09/093,585
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 08/464,590
; PRIOR FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 11
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-653-11

Query Match      100.0%; Score 268; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSLFLLLFFSHLLISAWAHGEKRLAPKQGPATDNPIGSSSSSSSSAMSSSSAS 60
DB 1 MSLSLFLLLFFSHLLISAWAHGEKRLAPKQGPATDNPIGSSSSSSSSAMSSSSAS 60
QY 61 SSPASLSGSGGLESGSPQWSPSGRRTGSLYCRVIGIHLQIYPDGKNGSHKANMLSV 120
DB 61 SSPASLSGSGGLESGSPQWSPSGRRTGSLYCRVIGIHLQIYPDGKNGSHKANMLSV 120
QY 121 LEIFAVSQGIVIGRVFSNKFPLAMSKGKGLHSAKFTDDCKRERFOENSNTTASAIHR 180
DB 121 LEIFAVSQGIVIGRVFSNKFPLAMSKGKGLHSAKFTDDCKRERFOENSNTTASAIHR 180
QY 181 TEKGTREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEQPELSTVTVPKQNP 240
DB 181 TEKGTREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEQPELSTVTVPKQNP 240
QY 241 SPIKSKIPLSAPRKNTNSVYKYLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVYKYLKFRFG 268

RESULT 11
US-10-037-922-33
; Sequence 33, Application US/10037922
; Publication No. US20040096936A1
; GENERAL INFORMATION:
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Raymond, Fenella
; APPLICANT: Bukowski, Thomas R.
; APPLICANT: Holderman, Susan D.
; APPLICANT: Hansen, Birgit
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
; FILE REFERENCE: 96-20
; CURRENT APPLICATION NUMBER: US/10/037,922
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 08/951,822
; PRIOR FILING DATE: 1997-10-16
```

```
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-922-33

Query Match      100.0%; Score 268; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSLFLLLFFSHLLISAWAHGEKRLAPKQGPATDNPIGSSSSSSSSAMSSSSAS 60
DB 1 MSLSLFLLLFFSHLLISAWAHGEKRLAPKQGPATDNPIGSSSSSSSSAMSSSSAS 60
QY 61 SSPASLSGSGGLESGSPQWSPSGRRTGSLYCRVIGIHLQIYPDGKNGSHKANMLSV 120
DB 61 SSPASLSGSGGLESGSPQWSPSGRRTGSLYCRVIGIHLQIYPDGKNGSHKANMLSV 120
QY 121 LEIFAVSQGIVIGRVFSNKFPLAMSKGKGLHSAKFTDDCKRERFOENSNTTASAIHR 180
DB 121 LEIFAVSQGIVIGRVFSNKFPLAMSKGKGLHSAKFTDDCKRERFOENSNTTASAIHR 180
QY 181 TEKGTREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEQPELSTVTVPKQNP 240
DB 181 TEKGTREMYVALNKGKAKRGCSPRVKPOHISTHFLPRKQSEQPELSTVTVPKQNP 240
QY 241 SPIKSKIPLSAPRKNTNSVYKYLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVYKYLKFRFG 268

RESULT 12
US-10-854-485-33
; Sequence 33, Application US/10854485
; Publication No. US20050043234A1
; GENERAL INFORMATION:
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
; FILE REFERENCE: 96-20C7
; CURRENT APPLICATION NUMBER: US/10/854,485
; PRIOR FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: 10/315,431
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10/081,347
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 09/634,318
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 09/613,708
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 09/574,750
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/229,947
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: 08/951,822
; PRIOR FILING DATE: 1997-10-16
; PRIOR APPLICATION NUMBER: 60/028,646
; PRIOR FILING DATE: 1996-10-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-854-485-33

Query Match      100.0%; Score 268; DB 5; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSLFLLLFFSHLLISAWAHGEKRLAPKQGPATDNPIGSSSSSSSSAMSSSSAS 60
```

Db 1 MSLSLFLLLPFSHLITLSAMAHGKRLAPKGPATDNPJGSSSRQSSSSAMSSSSAS 60
Qy 61 SSPASLSQSGSLQSSQSPSPSGRRTGSLYCRVIGIGHLOIYDCKNGSHENAMLSV 120
Db 61 SSPASLSQSGSLQSSQSPSPSGRRTGSLYCRVIGIGHLOIYDCKNGSHENAMLSV 120
Qy 121 LEIFAVSOGIVGIRGVFSNKFLLAMSKGKGLHSAKFTDCKRFRFOENSYNTYASAIHR 180
Db 121 LEIFAVSOGIVGIRGVFSNKFLLAMSKGKGLHSAKFTDCKRFRFOENSYNTYASAIHR 180
Qy 181 TEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOSEOPELSFTVTVPKKNP 240
Db 181 TEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOSEOPELSFTVTVPKKNP 240
Qy 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
Db 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
RESULT 13
US-10-413-537-10
Sequence 10, Application US/10413537
Publication No. US20050196842A1
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Roy, Margaret Ann
TITLE OF INVENTION: Polypeptides Sharing Sequence Identity With A Fibroblast Growth
TITLE OF INVENTION: Factor Polypeptide and Nucleic Acids Encoding The Same
FILE REFERENCE: P12191BCT
CURRENT APPLICATION NUMBER: US/10/413,537
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US 09/284,663
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 09/158,342
PRIOR FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: PCT/US98/25190
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,840
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 10
LENGTH: 268
TYPE: PRF
ORGANISM: Homo sapiens
US-10-413-537-10
Query Match 100.0%; Score 268; DB 5; Length 268;
Best Local Similarity 100.0%; Pred. No. 4,3e-240;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLSLFLLLPFSHLITLSAMAHGKRLAPKGPATDNPJGSSSRQSSSSAMSSSSAS 60
Db 1 MSLSLFLLLPFSHLITLSAMAHGKRLAPKGPATDNPJGSSSRQSSSSAMSSSSAS 60
Qy 61 SSPASLSQSGSLQSSQSPSPSGRRTGSLYCRVIGIGHLOIYDCKNGSHENAMLSV 120
Db 61 SSPASLSQSGSLQSSQSPSPSGRRTGSLYCRVIGIGHLOIYDCKNGSHENAMLSV 120
Qy 121 LEIFAVSOGIVGIRGVFSNKFLLAMSKGKGLHSAKFTDCKRFRFOENSYNTYASAIHR 180
Db 121 LEIFAVSOGIVGIRGVFSNKFLLAMSKGKGLHSAKFTDCKRFRFOENSYNTYASAIHR 180
Qy 181 TEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOSEOPELSFTVTVPKKNP 240
Db 181 TEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOSEOPELSFTVTVPKKNP 240
Qy 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
Db 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268

Db 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
RESULT 14
US-09-345-373-15
Sequence 15, Application US/09345373
Publication No. US20030077695A1
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RAMPEY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,373
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFER, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030077695A1 Relevant
TOPOLOGY: No. US20030077695A1 Relevant
MOLECULE TYPE: protein

Blank Page (USPTO)

GenCore version 5.1.7
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OW protein - protein search, using sw model

Run on: April 11, 2006, 03:33:26 ; Search time 73 Seconds
(without alignments)
2590.159 Million cell updates/sec

Title: US-10-089-485-4
Perfect score: 268
Sequence: 1 MSLSFLLLPFSHLITSAWA.....LSAPRKNTSVYKRLKPRFG 268

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	226	84.3	268	1	FGF5 HUMAN
2	195	72.8	268	2	Q8NPF50 HUMAN
3	94	35.1	125	2	Q8NMG6 HUMAN
4	90	33.6	264	1	FGF5 MOUSE
5	90	33.6	266	1	FGF5 RAT
6	77	28.7	129	2	Q6A549 HUMAN
7	60	22.4	153	2	Q8S073 CANFA
8	30	11.2	99	2	Q6XK01 RABIT
9	27	10.1	79	2	Q6XK00 RABIT
10	21	7.8	225	2	Q5TLE2 BRARE
11	19	7.1	230	2	Q4RPO6 TETNG
12	16	6.0	87	2	Q8MN07 CANFA
13	10	3.7	109	2	O13543 YEAST
14	10	3.7	349	2	Q7Y0C1 ORYSA
15	10	3.7	418	2	Q54TY7 DICDI
16	10	3.7	420	2	Q76853 DICDI
17	10	3.7	702	2	Q9V356 DROME
18	10	3.7	706	2	Q8S2H3 DROME
19	10	3.7	706	2	Q8EBR3 DROME
20	9	3.4	140	2	Q8S1P2 ORYSA
21	9	3.4	143	2	Q02276 CABEL
22	9	3.4	168	2	Q9J173 MOUSE
23	9	3.4	188	2	Q8S444 SORBI
24	9	3.4	209	2	Q5MFO8 DICLA
25	9	3.4	482	2	Q7S0U9 NEICR
26	9	3.4	492	2	Q4QBT7 LITWA
27	9	3.4	492	2	Q8BSDS MOUSE
28	9	3.4	495	2	Q5VZ18 HUMAN
29	9	3.4	526	2	Q9ZRH9 ORYSA
30	9	3.4	540	2	Q650Z7 ORYSA
31	9	3.4	553	2	Q7TML6 MOUSE

32	9	3.4	565	2	Q6Z9D7 ORYSA	Q6Z9D7 oryza sativ
33	9	3.4	648	2	Q6ZEY3 ORYSA	Q6ZEY3 oryza sativ
34	9	3.4	712	2	Q6FWG1 CANGA	Q6FWG1 candida gla
35	9	3.4	719	2	Q6DJ90 XENTR	Q6DJ90 xenopus tro
36	9	3.4	745	2	Q8BN18 DROME	Q8BN18 drosophila
37	9	3.4	749	2	Q8DAV3 VIBVU	Q8DAV3 vibrrio vuln
38	9	3.4	749	2	Q7MJ05 VIBVU	Q7MJ05 vibrrio vuln
39	9	3.4	751	1	KLHL1 MOUSE	Q9J174 mus musculi
40	9	3.4	751	2	Q8CCY1 MOUSE	Q8CCY1 mus musculi
41	9	3.4	751	2	Q505B3 MOUSE	Q505B3 mus musculi
42	9	3.4	758	2	Q5VTX3 MOUSE	Q5VTX3 mus musculi
43	9	3.4	860	2	Q6CJ18 KLULA	Q6CJ18 kluyveromyc
44	9	3.4	863	2	Q51IK1 MAGGR	Q51IK1 magnaporthe
45	9	3.4	979	2	Q23096 ARATH	Q23096 arabidopsis

ALIGNMENTS

RESULT 1
ID FGF5_HUMAN STANDARD; PRT; 268 AA.
AC P12034; Q75846;
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Fibroblast growth factor 5 precursor (FGF-5) (HBGF-5) (Smag-82).
GN Name=FGF5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RC TISSUE=Brain stem;
RX MEDLINE=91045929; PubMed=1700424;
RA Haub O., Drucker B., Goldfarb M.;
RT "Expression of the murine fibroblast growth factor 5 gene in the adult
RT central nervous system";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RX MEDLINE=89096942; PubMed=3211147;
RA Zhan X., Bates B., Hu X., Goldfarb M.;
RT "The human FGF-5 oncogene encodes a novel protein related to
RT fibroblast growth factors";
RL Mol. Cell. Biol. 8:3487-3495(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM SHORT).
RA Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A., Yoneda A., Komi A.,
RA Imanura T.;
RT "An alternatively-spliced FGF-5 mRNA is abundant in brain and
RT translates into a partial agonist/antagonist for FGF-5 neurotrophic
RT activity";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM SHORT).
RC TISSUE=umbilical artery;
RX MEDLINE=20379035; PubMed=10823842; DOI=10.1074/jbc.M910099199;
RA de Vries C.J.M., van Achterberg T.A.R., Horrevorts A.J.G.,
RA ten Cate U.W., Pannekoek H.;
RT "Differential display identification of 40 genes with altered
RT expression in activated human smooth muscle cells. Local expression in
RT atherosclerotic lesions of smags, smooth muscle activation-specific
RT genes";
RL J. Biol. Chem. 275:23939-23947(2000).
RN [5]
RP FUNCTION: This oncogene is expressed in neonatal brain. FGF-5 can
RP transform NIH 3T3 cells.
RN [6]
RP ALTERNATIVE PRODUCTS:
RN [7]
RP Event=Alternative splicing; Named isoforms=2;
RN [8]
RP Name=Long;
RN [9]
RP IsoId=P12034-1; Sequence=Displayed;

Oy		43	GSSSQSSSSANSSASSSPASIGSQSGGLEQSSFPQSPGSRRTGISYCRGIGHLQ	102
Dd		43	GSSSQSSSSANSSASSSPASIGSQSGGLEQSSFPQSPGSRRTGISYCRGIGHLQ	102
Oy		103	IYPDKVNGSHANMLSVLEIFAVSOGIIVGINGVFNKFLANSKKGLHASAFYDDCKF	162
Dd		103	IYPDKVNGSHANMLSVLEIFAVSOGIIVGINGVFNKFLANSKKGLHASAFYDDCKF	162
Oy		163	RRPFQENSNTNYASAIIHRTKTEGREMYVALNKRGAARCGSPRVKFOHISTHFLPRPKOS	222
Dd		163	RRPFQENSNTNYASAIIHRTKTEGREMYVALNKRGAARCGSPRVKFOHISTHFLPRPKOS	222
Oy		223	EOPELSFVTVEBK 237	
Dd		223	EOPELSFVTVEBK 237	
RESULT 3				
QBNSBG6_HUMAN				
ID	QBNSBG6_HUMAN	PRELIMINARY;	PRT,	125 AA.
AC	QBNSBG6;			
DT	01-OCT-2002	(TREMBLrel. 22, Created)		
DR	01-OCT-2002	(TREMBLrel. 22, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
Ds	Hypothetical protein FLJ33238.			
Os	Homo sapiens (Human).			
Oc	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
Oc	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;			
Ox	Homo.			
Rn	NCBI_Taxid=9606;			
Rp	[1]			
Rp	NUCLEOTIDE SEQUENCE.			
Rx	PubMed=14702039; DOI=10.1038/ng1285;			
Ra	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
Ra	Kamakura A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,			
Ra	Sekine M., Ohyashiki M., Nishi T., Shibaara T., Tanaka T., Ishii S.,			
Ra	Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,			
Ra	Nagaharti K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M.,			
Ra	Shigatori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,			
Ra	Sugawara M., Takahashi N., Kanda K., Yokoi T., Furuya T., Kikkawa E.,			
Ra	Omura Y., Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M.,			
Ra	Yamazaki M., Ninomiya K., Ichibashi T., Yamashita H., Murakawa K.,			
Ra	Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,			
Ra	Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotuta T.,			
Ra	Kusano J., Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O.,			
Ra	Nomura Y., Tojiwa S., Komai F., Hara R., Takeuchi K., Arita M.,			
Ra	Imose N., Museshino K., Yuuki H., Oshima A., Saeeki N., Aotsuka S.,			
Ra	Moriyaka Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			
Ra	Motiyasu S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,			
Ra	Nishiguchi H., Watanabe T., Sugiyama A., Takenoto M., Kawakami B.,			
Ra	Fujimoto Y., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
Ra	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,			
Ra	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
Ra	Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,			
Ra	Matsuura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,			
Ra	Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,			
Ra	Mizushima-Sugeno J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,			
Ra	Okumura K., Nagase T., Nomura N., Kikuchi H., Masuhito Y., Yamashita R.,			
Ra	Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,			
Rt	"Complete sequencing and characterization of 21,243 full-length human			
Rt	cDNAs"			
Rl	Nat. Genet. 36:40-45(2004).			
Dr	EMBL, AK090557; BAC03477.1; -; mRNA.			
Dr	HSSP, Q02195, IQCQ.			
Dr	GO; GO:0008083; F:growth factor activity; IEA.			
Dr	InterPro; IPRO02348; IL1_HBGF.			
Dr	Pfam; PF00167; FGF, 1..IL1_HBGF.			
Dr	PRINTS; PR00262; IL1HBGF.			
Dr	ProDom; PD000831; IL1_HBGF, 1.			
Dr	SMART; SM00442; FGF, 1.			
Dr	PROSITE; PS00247; HBGF_FGF; UNKNOWN 1.			

Seq	SEQUENCE	125 AA;	14536 MW;	EDB5B51C85B8BBCE	CNC64;
Qy	Query Match	35.14	Score 94;	DB 2;	Length 125;
Db	Best Local Similarity	100.04	Pred. No. 1.6e-63;		
Matches	94;	Conservative	0;	Mismatches	0;
Indels					
Gaps					
Qy	144	MSKGGKHLAASKKFPDDCKPRRRFQENSNNTYASAIHRTKGTGRMYVALNRRGKRRCS	203		
Db	1	MSKGGKHLAASKKFPDDCKPRRRFQENSNNTYASAIHRTKGTGRMYVALNRRGKRRCS	60		
Qy	204	PRVPRQHIHTHPLPRFKQSEQPELSFTVYDEKK	237		
Db	61	PRVPRQHIHTHPLPRFKQSEQPELSFTVYDEKK	94		
RESULT 4					
FGF5_MOUSE					
ID	RGFS_MOUSE	STANDARD;	PRF;	264 AA.	
AC	PI6566;	088825;			
DT	01-APR-1990	(Rel. 14, Created)			
DT	01-APR-1990	(Rel. 14, Last sequence update)			
DT	13-SEP-2005	(Rel. 48, Last annotation update)			
DE	Fibroblast growth factor 5 precursor (FGF-5) (HBGF-5).				
CN	Name=Rgfs; Synonyms=Rgf-5;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muroidea; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
LN	[1]				
RP	NCBI_EOTIDE SEQUENCE (ISOFORM LONG).				
RX	MEDLINE=90201563; PubMed=2318343;				
RA	Hebert J.M., Basillio C., Goldfarb M., Haub O., Martin G.R.;				
RT	"Isolation of cDNAs encoding four mouse FGF family members and				
RL	characterization of their expression patterns during embryogenesis.";				
LN	Dev. Biol. 138:454-463(1990).				
LN	[2]				
RP	NCBI_EOTIDE SEQUENCE (ISOFORM LONG).				
RC	STRAIN=C57BL/6;				
RX	MEDLINE=91045929; PubMed=1700424;				
RA	Haub O., Drucker B., Goldfarb M.;				
RT	"Expression of the murine fibroblast growth factor 5 gene in the adult				
RL	central nervous system.";				
LN	Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).				
LN	[3]				
RP	NCBI_EOTIDE SEQUENCE (ISOFORM SHORT).				
RX	MEDLINE=99003286; PubMed=9786339; DOI=10.1074/jbc.273.44.29262;				
RA	Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A.U., Yoneda A.,				
RA	Komi A., Imanura T.;				
RT	"An alternatively spliced fibroblast growth factor (FGF)-5 mRNA is				
RT	abundant in brain and translates into a partial agonist/antagonist for				
RT	FGF-5 neurotrophic activity.";				
RL	J. Biol. Chem. 273:29262-29271(1998).				
LN	[4]				
RP	NCBI_EOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).				
RC	STRAIN=C57BL/6J; TISSUE=Skin;				
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;				
RA	Kozaki Y., Furuno M., Kasukawa T., Adachi T., Bono H., Kondo S.,				
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,				
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,				
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Queckenbush U.,				
RA	Schmitt L.M., Knapin A., Matcudá H., Batalov S., Beisel K.W.,				
RA	Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.B., Cousins S.,				
RA	Dalla E., Drgant T.A., Fletcher C.F., Forrest A., Frazer K.S.,				
RA	Gaestlerland T., Gariboldi M., Glasi C., Godzik A., Gough J.,				
RA	Grimmond S., Guelinich S., Hirokawa N., Jackson I.U., Jarvis E.D.,				
RA	Kanai A., Kawai H., Kawasawa Y., Kédzieriski R.M., King B.L.,				
RA	Konagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,				
RA	Maglott D.R., Murochkin L., Marchionni L., McKenzie L., Miki H.,				
RA	Masushima T., Numa K., Okido T., Pavan W.C., Petrea G., Pesole G.,				
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,				
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,				
RA	Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,				

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmig L.G., Wymshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Atzawa K., Arakawa T., Fukuda S.,
 RA Hare A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 RN (5)
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.A., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Paney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- ALTERNATIVE PRODUCTS;
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P15656-1; Sequence=Displayed;
 CC Name=Short; Synonyms=RGF-5;
 CC IsoId=P15656-2; Sequence=VSP_001520; VSP_001521;
 CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, M30643; AAA86698.1; -; mRNA.
 CC EMBL, M37823; AAB02660.1; -; Genomic DNA.
 CC EMBL, M37821; AAB02660.1; JOINED; Genomic DNA.
 CC EMBL, M37822; AAB02660.1; JOINED; Genomic DNA.
 CC EMBL, M37821; AAB02659.1; ALT SEQ; Genomic DNA.
 CC EMBL, AB016516; BAA33737.1; -; mRNA.
 CC EMBL, AK028894; BAC26069.1; -; mRNA.
 CC EMBL, AK028894; BAC26179.1; -; mRNA.
 CC EMBL, BC071227; AAH71227.1; -; mRNA.
 CC PIR, A36207; A36207.
 CC HSSP, P08620; 110T.
 CC Ensembl, ENSMUSG00000029337; Mus musculus.
 CC MGI, MGI:95519; Rgf5.
 CC GO, GO:0005615; C:extracellular space; TAS.
 CC GO, GO:0010001; P:glial cell differentiation; IMP.
 CC InterPro, IPR002209; GF_heparin_bd.
 CC InterPro, IPR002348; ILI_HBGF.
 CC Pfam, PF00167; RGF_1.
 CC PRINTS, PR00263; HBGRFG.
 CC PRINTS, PR00262; ILIHBGF.
 CC PRODOM, PD000831; ILI_HBGF; 1.
 CC PROSITE, PS00247; HBGF_RGF; 1.

KW Alternative splicing; glycoprotein; growth factor; Mitogen;
 KW Proco-oncogene; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 264 Fibroblast growth factor 5.
 FT COMBINS 53 59 Poly-Ser. (GlcNAc...) (Potential).
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 118 121 ILI1 -> Q1YG (in isoform Short).
 FT VARSPLIC 122 264 /FTId=VSP_001520.
 FT VARSPLIC 264 264 Missing (in isoform Short).
 FT VARSPLIC 264 264 /FTId=VSP_001521.
 SQ SEQUENCE 264 AA; 29103 MW; F6A9C0153BB923D1 CRC64;
 Query Match 33.6%; Score 90; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 2.6e-79;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 121 LEIFAVSGGIGIRVFNKPLMSKKKTLASAKFTDDCKFRFRFQNSVYTAIAHR 180
 DB 119 LEIFAVSGGIGIRVFNKPLMSKKKTLASAKFTDDCKFRFRFQNSVYTAIAHR 178
 QY 181 TEKTRGVYVVALNKKRGKAKGCGSPVKKPOH 210
 DB 179 TEKTRGVYVVALNKKRGKAKGCGSPVKKPOH 208
 RESULT 5
 FGFS RAT
 ID FGFS RAT STANDARD; PRT; 266 AA.
 AC P48807; Q63402;
 DT 01-FEB-1996 (Rel. 33; Created)
 DT 01-FEB-1996 (Rel. 33; Last sequence update)
 DT 13-SEP-2005 (Rel. 48; Last annotation update)
 DE Fibroblast growth factor 5 precursor (FGF-5) (HBGF-5).
 GN Name=RGF5; Synonyms=RGF-5;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN (1)
 RN NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT).
 RC STRAIN=Miscar;
 RX MEDLINE=96201703; PubMed=8611621; DOI=10.1016/0167-4781(19)60001-1;
 RA Hattori Y., Yamasaki M., Itoh N.;
 RT "The rat FGF-5 mRNA variant generated by alternative splicing encodes
 RT a novel truncated form of FGF-5."
 RL Biochim. Biophys. Acta 1306:31-33 (1996).
 CC -1- ALTERNATIVE PRODUCTS;
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P48807-1; Sequence=Displayed;
 CC Name=Short; Synonyms=RGF-5;
 CC IsoId=P48807-2; Sequence=VSP_001522; VSP_001523;
 CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, D64085; BAA10966.1; -; mRNA.
 CC EMBL, D64086; BAA10967.1; -; mRNA.
 CC PIR, S68144; S68144.
 CC PIR, S68145; S68145.
 CC HSSP, P08620; 110T.
 CC Ensembl, ENSRNOG00000022631; Rattus norvegicus.
 CC RGD, 620129; Rgf5.
 CC GO, GO:0008083; F:growth factor activity; IDA.
 CC GO, GO:0005163; F:nerve growth factor receptor binding; TAS.
 CC GO, GO:0008283; P:cell proliferation; IDA.
 CC InterPro, IPR002209; GF_heparin_bd.
 CC InterPro, IPR002348; ILI_HBGF.

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DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR Altemative splicing; Glycoprotein; Growth factor; Mitogen;
KW Proto-oncogene; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 266 Fibroblast growth factor 5.
FT COMBIDAS 54 59 Poly-Ser.
FT CARBOHYD 108 108 N-linked (GLCNAC..)(Potential).
FT VARSPLIC 118 121 ILEI -> OIYR (in isoform short).
FT VARSPLIC 122 266 /FTID=VSP 001522.
FT VARSPLIC 266 Missing (in isoform short).
FT VARSPLIC /FTID=VSP 001523.
SQ SEQUENCE 266 AA; 29264 MW; 95B0A0CA7C0A200C CRC64;

Query Match
Best Local Similarity 100.0%; Score 90; DB 1; Length 266;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LEIPAVSGIVGIRGVFNKFLAMSKKGLHSAKFTDDCKRFRFQNSYNTYASAIHR 180
DB 119 LEIPAVSGIVGIRGVFNKFLAMSKKGLHSAKFTDDCKRFRFQNSYNTYASAIHR 178
QY 181 TEXTGREMYVALNKRKAKRGSGPRVYKPOH 210
DB 179 TEXTGREMYVALNKRKAKRGSGPRVYKPOH 208

RESULT 6
Q6A549_HUMAN PRELIMINARY; PRT; 129 AA.
AC Q6A549;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DR Fibroblast growth factor 5 isoform b'.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakakuki T., Ueba T.;
RL Submitted (FBI-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF355187; AAQ15127.1; -; mRNA.
DR GO; GO:0008083; F; growth factor activity; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR Prodom; PD000831; IL1_HBGF; 1.
SQ SEQUENCE 129 AA; 13509 MW; 98C791BBA754EA2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 77; DB 2; Length 129;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GSSSRSSSSAMSSSSPAAISGSSGSSFFQSPSGRRTGSLYCRVIGIFHLQ 102
DB 43 GSSSRSSSSAMSSSSPAAISGSSGSSFFQSPSGRRTGSLYCRVIGIFHLQ 102
QY 103 IYPDGKVGSHENMLIS 119
DB 103 IYPDGKVGSHENMLIS 119

RESULT 7
Q8SQ73_CANFA PRELIMINARY; PRT; 153 AA.
AC Q8SQ73;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FGF-5 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cartright J.M.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY074893; AAL82819.1; -; Genomic DNA.
DR EMBL; AY074892; AAL82819.1; JOINED; Genomic DNA.
DR HSSP; Q02195; 100K.
DR SMR; Q8SQ73; 163-223.
DR Ensemble; ENSCAFG0000008886; Canis familiaris.
DR GO; GO:0008083; F; growth factor activity; IEA.
DR InterPro; IPR002309; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF.
DR PRODOM; PD000831; IL1_HBGF.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
KW Growth factor.
FT NON_TER 1
SQ SEQUENCE 153 AA; 17420 MW; ABE13D0921376295 CRC64;

Query Match
Best Local Similarity 100.0%; Score 60; DB 2; Length 153;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LEIPAVSGIVGIRGVFNKFLAMSKKGLHSAKFTDDCKRFRFQNSYNTYASAIHR 180
DB 6 LEIPAVSGIVGIRGVFNKFLAMSKKGLHSAKFTDDCKRFRFQNSYNTYASAIHR 65

RESULT 8
Q6XK01_RABIT PRELIMINARY; PRT; 99 AA.
AC Q6XK01;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DR Fibroblast growth factor 5 (Fragment).
CN Name=RGFS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=rex;
RL Submitted (FBI-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY230008; AAF55849.1; -; mRNA.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10074 MW; DC2F2385BBD427B CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 99;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 PAASIGSGSGGLESGFFQSPSGRRTGSLY 92
DB 70 PAASIGSGSGGLESGFFQSPSGRRTGSLY 99

RESULT 9
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Q6XK00_RABIT
ID Q6XK00_RABIT PRELIMINARY; PRT; 79 AA.
AC Q6XK00;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Fibroblast growth factor 5 (Fragment).
GN Name=FGF5;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=rex;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY230009; AAP55850.1; -; mRNA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF_1; IL1_HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9056 MW; 8C50A729F49955E0 CRC64;

Query Match 10.1%; Score 27; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 TGEWTVVANKRGKARCGSPRYKPOH 210
Db 3 TGEWTVVANKRGKARCGSPRYKPOH 29

RESULT 10
Q5TLE2_BRABE PRELIMINARY; PRT; 225 AA.
ID Q5TLE2_BRABE;
AC Q5TLE2;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE FGF5.
GN Name=fgf5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Itch N.
RL "Danio rerio fibroblast growth factor 5 (fgf5) mRNA."
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB194699; BAD69616.1; -; mRNA.
DR ZFIN; ZDB-GENE-050201-6; fgf5.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF_1; IL1_HBGF.
DR PRINTS; PR00263; HBGF_FGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF_1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor.
SQ SEQUENCE 225 AA; 25933 MW; 329EAEDEB071308C CRC64;

Query Match 7.8%; Score 21; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 156 FTDDCKFRFRFGNSYNTYAS 176
Db 110 FTDDCKFRFRFGNSYNTYAS 130

RESULT 11
Q4RP06_TESTNG PRELIMINARY; PRT; 230 AA.
ID Q4RP06_TESTNG;
AC Q4RP06;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 12 SCAP15007, whole genome shotgun sequence.
GN (Fragment).
OS ORFNames=GSTENG00030976001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphae; Acanthopterygii; Percomorphae; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Catellico L., Poulet J., De Bernardis V.,
RA Blumont C., Skallil Z., Crottiello L., Poulet J., De Bernardis V.,
RA Cruaud C., Duprat S., Broctier P., Coultanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Querier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolious H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; GAB01015007; CAG09626.1; -; Genomic_DNA.
DR InterPro; IPR002209; GF_heparin_bd.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF_1; IL1_HBGF.
DR PRINTS; PR00263; HBGF_FGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF_1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor.
FT NON_TER 230
FT NON_TER 230
SQ SEQUENCE 230 AA; 26100 MW; 42BB6EDCE908BC0A CRC64;

Query Match 7.1%; Score 19; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.3e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 DDCKFRFRFGNSYNTYAS 176
Db 110 DDCKFRFRFGNSYNTYAS 128

RESULT 12
Q8WN07_CANPA PRELIMINARY; PRT; 87 AA.
ID Q8WN07_CANPA;
AC Q8WN07;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Fibroblast growth factor 5 (Fragment).
 GN Name=FGF-5;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 NC NCBL_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Carvirignt J.M.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF453760; AAL50825.1; -; Genomic_DNA.
 DR HSSP; P08620; 11UT.
 DR Ensembl; ENSCARG0000008885; Canis familiaris.
 DR GO; GO:0008083; F: growth factor activity; IEA.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR ProDom; PD000831; IL1_HBGF; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 87 AA; 8491 MW; 940B9B02538C38CF CRC64;
 Query Match 6.0%; Score 16; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 94 RVGIGFHLQIYPDGKV 109
 DB 72 RVGIGFHLQIYPDGKV 87
 RESULT 13
 ID 013543_YEAST
 AC 013543;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, last annotation update)
 DE YLR294CP (YLR294C).
 GN OrderedLocustNames=YLR294C;
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NC NCBL_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97313267; PubMed=9169871;
 RA Johnston M., Hillier L.W., Riles L., Albertmann K., Andre B.,
 RA Anstorge W., Beres V., Bruckner M., Delius H., Dubois E.,
 RA Duesterhoeft A., Shtian K.-D., Floeth M., Goffeau A., Hebling U.,
 RA Heumann K., Heuss-Neitzel D., Hilbert H., Higer F., Kleine K.,
 RA Koester P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T.,
 RA Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E.,
 RA Pohl T.M., Portetelle D., Purnelle B., Reumann S., Rieger M.,
 RA Rinke M., Rose M., Scharte M., Scherens B., Scholten P., Schwager C.,
 RA Schwarz S., Underwood A.P., Utterström L.A., Vandenbol M.,
 RA Verhaaselt P., Viereckels F., Voet M., Volckaert G., Voss H.,
 RA Wambutt R., Weller E., Weller H., Zimmermann F.K., Zollner A.,
 RA Hand J., Holsel J.D.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
 RL Nature 387:87-90(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Pauley A.;
 RN Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RN Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RA Cherry J.M.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Marischky G., Rolfs A., Richardson A., Kane M., Bagui M., Taycher E.,
 RA Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F.,
 RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
 RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
 RA Labaer J.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U17243; AAB67352.1; -; Genomic_DNA.
 DR EMBL; AY558218; AAS56544.1; -; Genomic_DNA.
 DR PIR; S69307; S69307.
 DR Interact; O13543; -;
 KW Complete proteome.
 SQ SEQUENCE 109 AA; 13120 MW; 02E1B166CFC70BEC CRC64;
 Query Match 3.7%; Score 10; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SLSEFLILFP 11
 DB 82 SLSEFLILFP 91
 RESULT 14
 ID 07Y0C1_ORYZA
 AC 07Y0C1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Putative DoF zinc finger protein.
 GN Name=OSJNB0079B15.26;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NC NCBL_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Ganberger K., Jones K.M.,
 RA Overton II L.L., Teltrin T., Kim M.M., Bera J.U., Jin S.S.,
 RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsieh J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Uteckback T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.D., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC099043; AAP50963.1; -; Genomic_DNA.
 DR Gramene; 07Y0C1; -;
 DR GO; GO:0003677; F: DNA binding; IEA.
 DR InterPro; IPR003851; ZnF_Dof.
 DR Pfam; PF02701; zf-Dof; 1.
 DR PROSITE; PS01361; zf_Dof_1; UNKNOWN_1.
 DR PROSITE; PS50884; zf_Dof_2; 1.
 SQ SEQUENCE 349 AA; 35653 MW; 7C8BBF28AC6CAF8 CRC64;
 Query Match 3.7%; Score 10; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 57 SSASSSPAS 66
 DB 249 SSASSSPAS 258
 RESULT 15
 OS4TY7_DICDI
 ID OS4TY7_DICDI PRELIMINARY; PRT; 418 AA.


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AC Q54TY7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE MADS-box transcription factor.
GN Name=srfA; ORFNames=DD80214892;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxId=4689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafrański K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Kontorov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Baeson N.,
RA Farbrother P., Desany B., Just B., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu W., Johnson D., Knights A.,
RA Loulèsed H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Christolm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFI01000074; EAL66675.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 418 AA; 47546 MW; 8C86042A75C82D8A CRC64;

Query Match 3.7%; Score 10; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 55 SSSSSASSSPA 64
DB 388 SSSSSASSSPA 397

```

Search completed: April 11, 2006, 03:36:41
 Job time : 73 secs

KW thrombocytopenic purpura; uveitis; retinal vasculitis; therapy.
 XX Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..268
 FT /note= "mature protein"
 XX
 XX MO9945952-A2.
 XX
 XX 16-SEP-1999.
 XX
 XX 10-MAR-1999; 99WO-US005375.
 XX
 XX 12-MAR-1998; 98US-00041383.
 XX
 XX 29-JAN-1999; 99US-00240952.
 XX
 XX (GENTH) GENTECH INC.
 XX
 XX KJ Javlin IJ, La Fleur M;
 PI
 DR WPI; 1999-561619/47.
 XX
 XX
 PT Novel method using FGF-5 for preventing retinal neuron death and for
 PT treating ocular diseases.
 XX
 XX Claim 3; Fig 10; 52pp; English.
 XX
 XX This sequence represents human fibroblast growth factor 5 (FGF-5),
 CC including the signal peptide. A claimed method of delaying, preventing or
 CC rescuing retinal cells from injury or death without causing angiogenesis
 CC or mitogenesis comprises administering an active FGF-5 polypeptide such
 CC as the present polypeptide. The retinal cells are: (a) retinal neurons
 CC selected from photoreceptors, retinal ganglion cells, displaced retinal
 CC ganglion cells, amacrine cells, displaced amacrine cells, horizontal and
 CC bipolar neurons; or (b) supportive cells selected from Muller cells and
 CC pigment epithelial cells. The method is used to treat photoreceptor cell
 CC injury or death caused by an ocular disease, retinal injury, light or
 CC environmental trauma. The ocular disease is especially selected from:
 CC retinitis pigmentosa; macular degeneration, including age-related;
 CC retinal detachment; retinal tears; retinopathy; retinal degenerative
 CC diseases; macular holes; degenerative myopia; acute retinal necrosis
 CC syndrome; traumatic choriorretinopathies or contusion, such as Purtscher's
 CC retinopathy; oedema; ischemic conditions such as central or branch
 CC retinal vision occlusion; collagen vascular diseases; thrombocytopenic
 CC purpura; uveitis; retinal vasculitis and occlusion associated with Eales
 CC disease and systemic lupus erythematosus (all claimed)
 XX
 XX Sequence 268 AA;
 SQ
 Query Match 88.4%; Score 237; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.4e-217;
 Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSLTLILFFSHLLISAWHGEKRLAPKQGPATDRNPRGSSSSSSSSSSSSSS 60
 DB 1 MSLSLTLILFFSHLLISAWHGEKRLAPKQGPATDRNPRGSSSSSSSSSSSSSS 60
 QY 61 SSPASLSQSGSLGSSPQSPGSRGSLYCRGIGIYDQKNGSHENMISV 120
 DB 61 SSPASLSQSGSLGSSPQSPGSRGSLYCRGIGIYDQKNGSHENMISV 120
 QY 121 LEIPAVSQIIVGIRGVFSNKLPLAMSKKGLHSAKFTDDCKRERFOENSYNTVASAIHR 180
 DB 121 LEIPAVSQIIVGIRGVFSNKLPLAMSKKGLHSAKFTDDCKRERFOENSYNTVASAIHR 180
 QY 161 TEKGRERYVALANKGKAKRGSSPRVKPOHISTHFLPRKQSGOPELSTTVTPPEKK 237
 DB 161 TEKGRERYVALANKGKAKRGSSPRVKPOHISTHFLPRKQSGOPELSTTVTPPEKK 237

RESULT 4
 AAB10296
 ID AAB10296 standard; protein; 268 AA.
 XX
 XX AAB10296;
 XX
 XX 20-NOV-2000 (first entry)
 XX
 XX Fibroblast growth factor FGFS protein SEQ ID NO: 15.
 XX
 XX Human; keratinocyte growth factor; KGF-2; antilucer; antidiabetic;
 KW antinflammatory; cytoprotective; dermatological; gastrointestinal;
 KW hepatic; respiratory; renal; cerebroprotective; mucositis; treatment;
 KW epithelial cell proliferation; inflammatory bowel disease; lung damage;
 KW liver disorder; diabetes; oral injury; gastrointestinal injury;
 KW gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft;
 KW skin disorder; renal failure; brain injury; intestinal fibrosis;
 KW proctitis; female reproductive tract disorder; pulmonary fibrosis;
 KW pneumonitis; pleural retraction; hemopoietic syndrome; myelotoxicity;
 KW fibroblast growth factor; FGFS.
 XX
 XX Undentified.
 XX
 XX US607692-A.
 XX
 XX 20-JUN-2000.
 XX
 XX 13-FEB-1998; 98US-00023082.
 XX
 XX 14-FEB-1995; 95WO-US001790.
 XX
 XX 05-JUN-1995; 95US-00461195.
 XX
 XX 13-AUG-1996; 96US-0023852P.
 XX
 XX 28-FEB-1997; 97US-0039045P.
 XX
 XX 23-MAY-1997; 97US-00862432.
 XX
 XX 13-AUG-1997; 97US-0055561P.
 XX
 XX 13-AUG-1997; 97US-00910875.
 XX
 XX (HUMA-) HUMAN GENOME SCL INC.
 XX
 XX Mendrick D, Duan DR, Ni J, Jimenez P, Coleman TA, Gruber JR;
 PI Dillon PJ, Gentz RL, Ruben SM, Zhang J, Moore PA, Rampy MA;
 PI
 DR WPI; 2000-441307/38.
 XX
 XX Novel keratinocyte growth factor useful for promoting and accelerating
 PT wound healing, comprising at least 10 contiguous amino acids from a
 PT specific amino acid sequence.
 XX
 XX Disclosure; Fig 2A-C; 190pp; English.
 XX
 XX This invention describes a novel human keratinocyte growth factor, KGF-2
 CC (1), which has antilucer, antidiabetic, antinflammatory, cytoprotective,
 CC dermatological, gastrointestinal, hepatic, respiratory, renal and
 CC cerebroprotective activity. (1) is useful for stimulating epithelial cell
 CC proliferation in patients suffering from wound, mucositis, ulcer such as
 CC venous stasis ulcer, diabetic ulcer and cubitus ulcer. (1) is also useful
 CC for treating inflammatory bowel disease, liver disorder, lung damage,
 CC diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric
 CC ulcer, duodenal ulcer, epidermolysis bullosa, skin graft, skin disorder,
 CC female failure, brain injury, breast tissue injury, urothelial damage,
 CC female reproductive tract disorder, intestinal fibrosis, proctitis,
 CC pulmonary fibrosis, pneumonitis, pleural retraction, hemopoietic syndrome
 CC and myelotoxicity. (1) is also useful for increasing the adherence of
 CC skin grafts to wound beds and to stimulate re-epithelialization from the
 CC wound bed, to produce changes in hepatocyte proliferation, to reduce the
 CC side effects of gut toxicity, to regenerate skin in full and partial
 CC thickness skin defects, and to prevent and heal damage to lungs. KGF-2
 CC shows enhanced activity, increased stability, higher yield and better
 CC solubility. This sequence represents the fibroblast growth factor FGFS
 CC which is described in the method of the invention
 XX
 XX Sequence 268 AA;
 SQ

Query Match 88.4%; Score 237; DB 3; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.4e-217;
 Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFFSHLLISAMAHGEKRLAPGPGPATDNRNPGSSSRQSSSSAMSSSSNS 60
 DB 1 MSLSFLLLFFSHLLISAMAHGEKRLAPGPGPATDNRNPGSSSRQSSSSAMSSSSNS 60
 QY 61 SSPASISLQSGSGLEQSSFWSPSGRRTGSLYCRVGIGFHLQIYDGVKNGSHEANMLSV 120
 DB 61 SSPASISLQSGSGLEQSSFWSPSGRRTGSLYCRVGIGFHLQIYDGVKNGSHEANMLSV 120
 QY 121 LEIFAVSGIYVIRGVFNKFLAMSKKGLHASAKFTDDCKFRERFOENSNTYVASAIHR 180
 DB 121 LEIFAVSGIYVIRGVFNKFLAMSKKGLHASAKFTDDCKFRERFOENSNTYVASAIHR 180
 QY 181 TEKTRERYVALNKGKAKRGCSPRVKPQHISTHFLPRFKOSEBELSFTYVPEKK 237
 DB 181 TEKTRERYVALNKGKAKRGCSPRVKPQHISTHFLPRFKOSEBELSFTYVPEKK 237

RESULT 5
 AAB61660
 ID AAB61660 standard; protein; 268 AA.
 AC AAB61660;
 XX 10-APR-2001 (first entry)
 DT FGFS protein.
 DE Keratinocyte growth factor; KGF-2; epithelial cell proliferation; wound;
 KW mucositis; ulcer; inflammatory bowel disease; liver disorder;
 KW lung damage; diabetes; oral injury; gastrointestinal injury;
 KW epidermolysis bullosa; renal failure; brain injury; proctitis;
 KW pulmonary fibrosis; haemopoietic syndrome; ovary injury; infertility;
 KW liver fibrosis.
 XX Homo sapiens.
 OS
 XX WO200102433-A1.
 PN 11-JAN-2001.
 PD 03-JUL-2000; 2000WO-US018328.
 PF 02-JUL-1999; 99US-0142343P.
 PR 14-JUL-1999; 99US-0143648P.
 PR 15-JUL-1999; 99US-0144024P.
 PR 12-AUG-1999; 99US-0146628P.
 PR 19-AUG-1999; 99US-0149935P.
 PR 03-NOV-1999; 99US-0163375P.
 PR 22-DEC-1999; 99US-0171677P.
 PR 19-APR-2000; 2000US-0198322P.
 PR 19-MAY-2000; 2000US-0205417P.
 PR 30-JUN-2000; 2000US-00142343.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;
 PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;
 XX WPI; 2001-071578/08.
 DR A polynucleotide encoding the human keratinocyte growth factor useful for
 PT stimulating epithelial cell proliferation in a patients that has e.g a
 PT wound.
 XX Discloure; Fig 2; 591pp; English.
 XX The present invention relates to human keratinocyte growth factor (KGF-2;
 CC see AAFJ1901 and AAB61657). The present sequence is a protein used in a
 CC sequence homology comparison with human KGF-2. KGF-2 can be used to

CC stimulate epithelial cell proliferation in a patient, where the patient
 CC has a wound, mucositis, diabetes, oral injury, inflammatory bowel disease, liver
 CC disorder, lung damage, diabetes, oral injury, gastrointestinal injury,
 CC gut toxicity, epidermolysis bullosa, skin graft, skin disorder, renal
 CC failure, brain injury, breast tissue injury, urothelial damage, female
 CC reproductive tract disorder, intestinal fibrosis, proctitis, pulmonary
 CC fibrosis, pneumonitis, plural retraction, haemopoietic syndrome, and
 CC myelotoxicity. In addition, KGF-2 can be used in the treatment or
 CC prevention of ovary injury, infertility, or fibrosis of the liver. KGF-2
 CC also promotes internal healing, donor site healing, internal surgical
 CC wound healing or healing of incisional wounds made during cosmetic
 CC surgery in a patient
 CC SQ Sequence 268 AA;

Query Match 88.4%; Score 237; DB 4; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.4e-217;
 Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFFSHLLISAMAHGEKRLAPGPGPATDNRNPGSSSRQSSSSAMSSSSNS 60
 DB 1 MSLSFLLLFFSHLLISAMAHGEKRLAPGPGPATDNRNPGSSSRQSSSSAMSSSSNS 60
 QY 61 SSPASISLQSGSGLEQSSFWSPSGRRTGSLYCRVGIGFHLQIYDGVKNGSHEANMLSV 120
 DB 61 SSPASISLQSGSGLEQSSFWSPSGRRTGSLYCRVGIGFHLQIYDGVKNGSHEANMLSV 120
 QY 121 LEIFAVSGIYVIRGVFNKFLAMSKKGLHASAKFTDDCKFRERFOENSNTYVASAIHR 180
 DB 121 LEIFAVSGIYVIRGVFNKFLAMSKKGLHASAKFTDDCKFRERFOENSNTYVASAIHR 180
 QY 181 TEKTRERYVALNKGKAKRGCSPRVKPQHISTHFLPRFKOSEBELSFTYVPEKK 237
 DB 181 TEKTRERYVALNKGKAKRGCSPRVKPQHISTHFLPRFKOSEBELSFTYVPEKK 237

RESULT 6
 ABP54276
 ID ABP54276 standard; protein; 268 AA.
 AC ABP54276;
 XX 16-JAN-2003 (first entry)
 DT Human fibroblast growth factor 5 protein SEQ ID NO.15.
 DE Human fibroblast growth factor 5 protein SEQ ID NO.15.
 XX Keratinocyte growth factor 2; KGF-2; fibroblast growth factor 12; FGF-12;
 KW KGF-2 Delta28; inflammation; vulnary; dermatological;
 KW pulmonary epithelial cell; mucositis; epidermolysis bullosa;
 KW wound healing.
 XX Homo sapiens.
 OS
 XX WO200277155-A2.
 PN 03-OCT-2002.
 PD 04-JAN-2002; 2002WO-US000101.
 PF 08-JAN-2001; 2001US-0259853P.
 PR 26-APR-2001; 2001US-0286368P.
 PR 09-NOV-2001; 2001US-0331168P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;
 PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;
 XX WPI; 2003-018897/01.
 DR Treating inflammation comprises administering Keratinocyte Growth Factor
 PT -2Delta28 to a patient.
 XX

PS Disclosure; Fig 2; 583pp; English.

XX
XX The present invention describes a method for treating inflammation. The
CC method comprises administering keratinocyte growth factor 2 (KGF-2)
CC Delta28 to a patient. Also described: (1) a method for stimulating the
CC growth of pulmonary epithelial cells; or (2) a method of preventing
CC mucositis. KGF-2 Delta28 has vulnerary and dermatological activities, and
CC can be used in gene therapy. KGF-2 Delta28 is useful for treating
CC inflammation, stimulating the growth of pulmonary epithelial cells or
CC preventing mucositis. It can also be used for treating epidermolysis
CC bullosa and for promoting wound healing. AB082994 to AB083130 and
CC ABP54273 to ABP54311 represent sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 268 AA;

Query Match 88.4%; Score 237; DB 6; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.4e-217;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLPFSLHLLISAWAHGKRLAPKGGPAPATDNNPSSSSSSSSSSSSSSSS 60
DB 1 MSLSFLLLPFSLHLLISAWAHGKRLAPKGGPAPATDNNPSSSSSSSSSSSSSSSS 60
QY 61 SSPASISGSGSGLEQSSPQSPGRRGSLYCRVIGIHFHLLQIYDPGKNGSHEANMLSV 120
DB 61 SSPASISGSGSGLEQSSPQSPGRRGSLYCRVIGIHFHLLQIYDPGKNGSHEANMLSV 120
QY 121 LEIFAVSGGIVGIRGVFNSKFLAMSKKGLASAKFTDDCKRERFQENSNTYTSALHR 180
DB 121 LEIFAVSGGIVGIRGVFNSKFLAMSKKGLASAKFTDDCKRERFQENSNTYTSALHR 180
QY 181 TKTGRBMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSBOPELSTFTVPEKK 237
DB 181 TKTGRBMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSBOPELSTFTVPEKK 237

RESULT 7
ADA95451
ID ADA95451 standard; protein; 268 AA.
XX
XX ADA95451;
AC
XX
DT 20-NOV-2003 (first entry)
XX
DB Fibroblast growth factor (FGF) polypeptide #3.
XX
XX Keratinocyte growth factor 2; KGF-2; epidermal cell; keratinocyte;
KW wrinkle; aged skin; skin strength; epidermal thickening;
KW scarring reduction; cosmetic surgery; epithelial cell; liver; pancreas;
KW kidney; prostate; bladder; lung; oesophagus; wound healing; diabetes;
KW ischaemic blockage; ischaemic injury; steroid; uraemia; malnutrition;
KW vitamin deficiency; obesity; immunosuppression; radiation therapy;
KW chemotherapy; anaesthetics; ulcer; burn; mucositis;
KW inflammatory bowel disease; inflammation; radiation-induced condition;
KW viral hepatitis; liver failure; pancreatitis; lung damaging condition;
KW renal failure; fibroblast growth factor; FGF.
XX
XX Unidentified;
OS
XX
PN US2003077695-A1.
XX
PD 24-APR-2003.
XX
XX 01-JUL-1999; 99US-00345373.
PF
XX
PR 14-FEB-1995; 95WO-US001790.
PR 13-AUG-1996; 96US-0023852P.
PR 28-FEB-1997; 97US-0039405P.
PR 23-MAY-1997; 97US-00862432.
PR 13-AUG-1997; 97US-005561P.
PR 13-AUG-1997; 97US-00910875.
PR 13-FEB-1998; 98US-00023082.
XX

XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;
PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;
XX WPI; 2003-596836/56.
DR
PT New Keratinocyte Growth Factor (KGF-2) polypeptides and polynucleotides,
PT useful for treating or preventing mucositis or Cronh's disease, reducing
PT scarring, or improving wound healing or skin strength.
XX
XX Disclosure; Fig 2; 195pp; English.

CC The invention relates to Keratinocyte Growth Factor 2 (KGF-2)
CC polypeptides and the polynucleotides encoding them. The KGF-2
CC polypeptides are useful for stimulating the proliferation of epidermal
CC cells (e.g. keratinocytes) to prevent or improve the appearance of
CC wrinkles or aged skin, improve skin strength, promote epidermal
CC thickening, reduce scarring or improve healing after cosmetic surgery.
CC The KGF-2 polypeptide is also useful for stimulating epithelial cells.
CC (e.g. epithelial cells of the liver, pancreas, kidney, prostate, bladder,
CC lung or oesophagus) or promoting wound healing in a wound healing
CC impaired individual (due to diabetes, ischaemic blockage or injury,
CC steroids, non-steroid compounds, uraemia, malnutrition, vitamin
CC deficiencies, obesity, infection, immunosuppression, radiation therapy or
CC chemotherapy). The wound may be caused by surgery (e.g. colonic or
CC gastrointestinal surgical procedures such as anastomosis), ulcers, burns,
CC etc. The KGF-2 polypeptide is also useful for treating or preventing
CC mucositis (e.g. oral, oesophageal, gastric or rectal), inflammatory bowel
CC disease (e.g. ulcerative colitis or Cronh's disease), inflammation (e.g.
CC psoriasis, eczema, dermatitis or arthritis), a radiation-induced
CC condition (e.g. oral injury, pulmonary fibrosis, myelotoxicity), viral
CC hepatitis, liver failure (caused by e.g. hepatitis, cirrhosis),
CC pancreatitis, lung damaging conditions (e.g. emphysema, lung cancer,
CC asthma), or renal failure. The polypeptide is further useful for
CC promoting hair growth, treating tissue exposed to radiation (e.g.
CC radiation for treating malignancy) or protecting tissue to be exposed to
CC radiation, or promoting tissue growth or repair. This sequence represents
CC a fibroblast growth factor (FGF) polypeptide of the invention.
XX
SQ Sequence 268 AA;

Query Match 88.4%; Score 237; DB 6; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.4e-217;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLPFSLHLLISAWAHGKRLAPKGGPAPATDNNPSSSSSSSSSSSSSSSS 60
DB 1 MSLSFLLLPFSLHLLISAWAHGKRLAPKGGPAPATDNNPSSSSSSSSSSSSSSSS 60
QY 61 SSPASISGSGSGLEQSSPQSPGRRGSLYCRVIGIHFHLLQIYDPGKNGSHEANMLSV 120
DB 61 SSPASISGSGSGLEQSSPQSPGRRGSLYCRVIGIHFHLLQIYDPGKNGSHEANMLSV 120
QY 121 LEIFAVSGGIVGIRGVFNSKFLAMSKKGLASAKFTDDCKRERFQENSNTYTSALHR 180
DB 121 LEIFAVSGGIVGIRGVFNSKFLAMSKKGLASAKFTDDCKRERFQENSNTYTSALHR 180
QY 181 TKTGRBMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSBOPELSTFTVPEKK 237
DB 181 TKTGRBMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSBOPELSTFTVPEKK 237

RESULT 8
ADD66124
ID ADD66124 standard; protein; 268 AA.
XX
XX ADD66124;
AC
XX
DT 15-JAN-2004 (first entry)
XX
DE Fibroblast growth factor, FGFS.

XX Fibrinolytic growth factor; keratinocyte growth factor-2; KGF-2;
 KW epidermal cell proliferation; epithelial cell proliferation;
 KW wound healing; colonic surgery; gastrointestinal surgery; mucositis;
 KW inflammatory bowel disease; inflammation; hair growth; radiation damage;
 KW tissue growth; female genital tract repair; urothelial healing;
 KW viral hepatitis; liver failure; pancreatitis; lung damaging condition;
 KW renal failure.
 XX Unidentified.
 OS
 XX US2003129687-A1.
 PD 10-JUL-2003.
 XX
 PF 15-FEB-2002; 2002US-00075446.
 XX
 PR 14-FEB-1995; 95MO-US001790.
 PR 05-JUN-1995; 95US-00461195.
 PR 13-AUG-1996; 96US-0023852P.
 PR 28-FEB-1997; 97US-0039045P.
 PR 13-AUG-1997; 97US-0055561P.
 PR 13-FEB-1998; 97US-00910875.
 PR 01-JUL-1999; 98US-00023082.
 XX
 PA (RUBEN/) RUBEN S M.
 PA (JIMENEZ/) JIMENEZ P.
 PA (DUAN/) DUAN D R.
 PA (RAMPE/) RAMPE M A.
 PA (MEND/) MENDRICK D.
 PA (ZHANG/) ZHANG J.
 PA (NIJ/) NI J.
 PA (MOOR/) MOORE P A.
 PA (COLE/) COLEMAN T A.
 PA (GRUB/) GRUBER J R.
 PA (DILL/) DILLON P J.
 PA (GENT/) GENTZ R L.
 XX
 PI Ruben SM, Jimenez P, Duan DR, Rampe MA, Mendrick D, Zhang J;
 PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;
 DR WPI, 2003-829563/77.
 XX
 PT New Keratinocyte Growth Factor-2 (KGF-2) polypeptide, useful for
 PT preparing a composition for reducing inflammation, promoting wound
 PT healing, hair growth, or treating or preventing liver or renal failure or
 PT pancreatitis.
 PS Disclosure; SEQ ID NO 15; 183bp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a sequence
 CC having 95% identity with amino acid residues 138(Gly)-208(Ser), 123(Val)-
 CC 208(Ser), 104(Glu)-208(Ser), 77(Val)-208(Ser), 69(Ser)-208(Ser), 63(Ala)-
 CC 208(Ser), 37(Cys)-208(Ser), 36(Thr)-208(Ser), 21(Tyr)-208(Ser), 63(Ala)-
 CC 153(Lys), 36(Thr)-153(Lys) or 138(Gly)-208(Ser) of human keratin growth
 CC factor-2 (KGF-2) appearing as ADB6111. Also included are an isolated
 CC polynucleotide encoding the polypeptide, a method of making a recombinant
 CC vector, a method of making a recombinant host cell, a recombinant host
 CC cell, a recombinant vector, a method of producing the polypeptide, a
 CC method of stimulating proliferation of epidermal cells, a method of
 CC stimulating proliferation of epithelial cells, a method of promoting
 CC wound healing, a method of treating wounds caused by a colonic or
 CC gastrointestinal surgical procedure, a method of treating or preventing
 CC mucositis, a method of treating inflammatory bowel disease, a method of
 CC reducing inflammation, a method of promoting hair growth, a method of
 CC treating tissue exposed to radiation or protecting tissue to be exposed
 CC to radiation, a method of promoting tissue growth or repair in the female
 CC genital tract, a method of promoting urothelial healing, a method of
 CC treating or preventing viral hepatitis, liver failure, pancreatitis, lung
 CC damaging condition or renal failure. The polypeptide is useful for
 CC preparing a composition for reducing inflammation, promoting wound or
 CC urothelial healing, hair growth, tissue growth or repair in the female

CC genital tract, treating tissue exposed to radiation or protecting tissue
 CC to be exposed to radiation, or treating or preventing viral hepatitis,
 CC liver or renal failure, pancreatitis or lung damaging condition. The
 CC present represents a fibroblast growth factor showing sequence similarity
 CC to human KGF-2 protein.

XX Sequence 268 AA;

Query Match 88.4%; Score 237; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2,4e-217;
 Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFFSHLLISAWHGEKRLAPKGPATTRNPRGSSRSSSSAMSSSAS 60
 DB 1 MSLSFLLLFFSHLLISAWHGEKRLAPKGPATTRNPRGSSRSSSSAMSSSAS 60
 QY 61 SSPASISGSGSGEFOSSPQWSPGSRGSLCYCRGIDPHLQIYDGVNGSHENMLSV 120
 DB 61 SSPASISGSGSGEFOSSPQWSPGSRGSLCYCRGIDPHLQIYDGVNGSHENMLSV 120
 QY 121 LEIFAVSGGIVGIRGVFNKPLAMSKKGLHASAKFTDCKRERFOENSYTTVASAIR 180
 DB 121 LEIFAVSGGIVGIRGVFNKPLAMSKKGLHASAKFTDCKRERFOENSYTTVASAIR 180
 QY 181 TEKTRREMYVALNKKKAKRGCSPRVKPQHISTHFLPRFKOSEDELSFTTVPEKK 237
 DB 181 TEKTRREMYVALNKKKAKRGCSPRVKPQHISTHFLPRFKOSEDELSFTTVPEKK 237

RESULT 9
 ADT97922
 ID ADT97922 standard; protein; 268 AA.
 XX
 AC ADT97922;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human keratinocyte growth factor-related FGF5 protein sequence SeqID15.

XX lung epithelial cell; cell proliferation stimulation; hyperkeratosis;
 KW buccal mucosa; tongue; oesophagus; keratinocyte growth factor; KGF-2;
 KW keratolytic; respiratory-Gen; lung disease; lung damage; emphysema;
 KW inhalation injury; hyaline membrane disease;
 KW infant respiratory distress syndrome; bronchopulmonary dysplasia;
 KW lung fibrosis; human; fibroblast growth factor; FGF.
 XX

OS Homo sapiens.

XX AU2003236478-A1.

XX 18-SEP-2003.

XX 26-AUG-2003; 2003AU-00236478.

XX 26-AUG-2003; 2003AU-00236478.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rampe M, Jimenez P, Louie A, Russell D, Mendrick D,
 PI WPI, 2004-662619/65.

XX Stimulating (M1) proliferation of lung epithelial cells, or inducing
 PT hyperkeratosis of the buccal mucosa, tongue and oesophagus, by
 PT administering to individual polypeptide having specific amino acid
 PT residues of keratinocyte growth factor.

XX Disclosure; SEQ ID NO 15; 330bp; English.

XX This invention relates to a novel method of stimulating proliferation of
 CC lung epithelial cells, or inducing hyperkeratosis of the buccal mucosa,
 CC tongue and oesophagus. The method involves administering to an individual
 CC a polypeptide comprising an amino acid sequence having amino acid

CC residues Arg(80)-Ser-(208), Val(77)-Ser(208), Cys(37)-Ser(208), Thr(36)-
CC Ser(208) or Met(1)-Ser(208) of fully defined sequence of keratinocyte
CC growth factor (KGF-2) having 208 amino acids as given in specification.
CC The invention may be useful for the production of compounds with a
CC keratolytic or respiratory-gen activity. The method is useful for
CC stimulating proliferation of lung epithelial cells, or inducing
CC hyperkeratosis of the buccal mucosa, tongue and oesophagus, where the
CC polypeptide is administered to treat or prevent lung diseases or lung
CC damage. The lung disease is acute or chronic lung disease, emphysema,
CC inhalation injuries, hyaline membrane disease, infant respiratory
CC distress syndrome or bronchiolopulmonary dysplasia. The lung damage is
CC caused by lung fibrosis. The method enables stimulation of proliferation
CC of lung epithelial cells, or induction of hyperkeratosis of the buccal
CC mucosa, tongue and oesophagus. The present sequence is that of a
CC fibroblast growth factor (FGF) protein which was used to demonstrate
CC homology to the human KGF protein which may be used in the method of the
CC invention.

CC Sequence 268 AA;

Query Match 88.4%; Score 237; DB 8; Length 268;

Best Local Similarity 100.0%; Pred. No. 2.4e-217;

Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFTLLIFPSHLILSAMHGEKRLAPGPGPAATDNPNGSSSSROSSSAMSSSAS 60
DB 1 MSLSFTLLIFPSHLILSAMHGEKRLAPGPGPAATDNPNGSSSSROSSSAMSSSAS 60
QY 61 SSPASISGSGSGLEQSSSFQMSPSGRRTGSLYCRVIGIYDYGKNGSHEANMLSV 120
DB 61 SSPASISGSGSGLEQSSSFQMSPSGRRTGSLYCRVIGIYDYGKNGSHEANMLSV 120
QY 121 LEIFAVSQGIVGIRGVFSNFKFLAMSKKGLHSAKFTDDCKRERFQENSYNTTASAIHR 180
DB 121 LEIFAVSQGIVGIRGVFSNFKFLAMSKKGLHSAKFTDDCKRERFQENSYNTTASAIHR 180
QY 181 TKTGREWVALNKGKAKRGCSPRVXQPHISTHFLPRFKOSEOPELSTTVVPEKK 237
DB 181 TKTGREWVALNKGKAKRGCSPRVXQPHISTHFLPRFKOSEOPELSTTVVPEKK 237

RESULT 10

ADK69307
ID ADK69307 standard; protein; 268 AA.

XX ADK69307;

XX 05-MAY-2005 (first entry)

XX Human heparin binding protein #7.

XX Heparin binding protein; Neuroprotective; Nootropic; Antiparkinsonian;
XX Anticonvulsant; VEGF-3 receptor; Angiogenesis stimulator; Gene Therapy;
XX vascular endothelial growth factor receptor 3; VEGFR-3;
XX angiogenesis disorder; neurodegenerative disorder; Alzheimer's disease;
XX Parkinson's disease; motor neuron disease; dementia; paralyisis; VEGF-C;
XX neurological disease; Huntingtons chorea;
XX vascular endothelial growth factor receptor 3; neurological disease.

XX Homo sapiens.

XX WO2005016963-A2.

XX 24-FEB-2005.

XX 14-JUN-2004; 2004WO-US019122.

XX 12-JUN-2003; 2003US-0478114P.

XX 12-JUN-2003; 2003US-0478390P.

XX 23-SEP-2003; 2003US-00669176.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (LUDW-) LICENTIA LTD.

XX Altralo K, He Y, Tammela T;
PI WPI; 2005-182331/19.
DR New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands
PT comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for
PT treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or
PT Huntington's disease.

PS Disclosure; SEQ ID NO 27; 219pp; English.

XX The invention relates to heparin-binding vascular endothelial growth
XX factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The
XX heparin binding VEGFR-3 proteins are used for stimulating
XX lymphangiogenesis or angiogenesis in a mammal, and for modulating the
XX growth of mammalian endothelial cells, mammalian endothelial precursor
XX cells or hematopoietic progenitor cells. The polypeptide may also be used
XX for promoting recruitment, proliferation, differentiation, migration or
XX survival of neuronal cells or neuronal precursor cells, and for treating
XX neurodegenerative disorder, e.g. Alzheimer's disease, Parkinson's
XX disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral
XX Sclerosis (ALS), dementia, or cerebral palsy. The present sequence
XX represents a human heparin binding protein of the invention.

XX Sequence 268 AA;

Query Match 88.4%; Score 237; DB 9; Length 268;

Best Local Similarity 100.0%; Pred. No. 2.4e-217;

Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFTLLIFPSHLILSAMHGEKRLAPGPGPAATDNPNGSSSSROSSSAMSSSAS 60
DB 1 MSLSFTLLIFPSHLILSAMHGEKRLAPGPGPAATDNPNGSSSSROSSSAMSSSAS 60
QY 61 SSPASISGSGSGLEQSSSFQMSPSGRRTGSLYCRVIGIYDYGKNGSHEANMLSV 120
DB 61 SSPASISGSGSGLEQSSSFQMSPSGRRTGSLYCRVIGIYDYGKNGSHEANMLSV 120
QY 121 LEIFAVSQGIVGIRGVFSNFKFLAMSKKGLHSAKFTDDCKRERFQENSYNTTASAIHR 180
DB 121 LEIFAVSQGIVGIRGVFSNFKFLAMSKKGLHSAKFTDDCKRERFQENSYNTTASAIHR 180
QY 181 TKTGREWVALNKGKAKRGCSPRVXQPHISTHFLPRFKOSEOPELSTTVVPEKK 237
DB 181 TKTGREWVALNKGKAKRGCSPRVXQPHISTHFLPRFKOSEOPELSTTVVPEKK 237

RESULT 11

AA31791
ID AA31791 standard; protein; 248 AA.

XX AA31791;

XX 06-DEC-1999 (first entry)

XX Human fibroblast growth factor 5 mature polypeptide.

XX Fibroblast growth factor 5; FGF-5; human; eye; retina; ocular disease;
XX retinopathy; maculopathy; retinal degeneration; retinitis pigmentosa;
XX macular degeneration; retinal detachment; retinal tear; macular hole;
XX degenerative myopia; acute retinal necrosis syndrome;
XX traumatic choroidretinopathy; Patacher's retinopathy; oedema;
XX retinal vision occlusion; collagen vascular disease;
XX thrombocytopenic purpura; uveitis; retinal vasculitis; therapy.

XX Homo sapiens.

XX WO945952-A2.

XX 16-SEP-1999.

XX 10-MAR-1999; 99WO-US005375.

AC AAE0639;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Human fibroblast growth factor-5 (FGF-5) peptide #1 from clone 6A4-1.
 XX
 KM Human; fibroblast growth factor-5; FGF-5; neoplasm; cytostatic; RCC;
 KM renal cell carcinoma; immunomodulator; gene therapy; carcinoma; breast;
 KM prostate; bladder; pancreas; TAA; tumour associated antigen;
 KM horseshoe kidney; Hipbel-Lindau disease; acquired renal cystic disease;
 KM adult polycystic kidney disease; clone 6A4-1.
 XX
 OS Homo sapiens.
 XX
 PN WO200125271-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 29-SEP-2000; 200WO-US026689.
 XX
 PR 02-OCT-1999; 99US-0157103P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Hanada K, Yang JC;
 XX
 DR WPI: 2001-290607/30.
 XX
 DR N-PSDB; AAD03937.
 XX
 PT Treating a subject having a neoplasm expressing fibroblast growth factor-
 PT 5 (FGF-5), e.g. prostate, breast, bladder, or pancreas carcinoma,
 PT comprises modulating an immune response to FGF-5 or modulating FGF-5
 PT expression or activity.
 XX
 PS Claim 7; Page 92; 101p; English.
 XX
 CC The present invention relates to a method for treating a subject having
 CC neoplasm expressing fibroblast growth factor-5 (FGF-5) comprises
 CC modulating an immune response to FGF-5 or FGF-5 expression or activity.
 CC FGF is a tumour associated antigen (TAA). The method is useful for
 CC treating or preventing a neoplasm such as prostate carcinoma, breast
 CC carcinoma, bladder carcinoma, pancreas carcinoma, and renal cell
 CC carcinoma (RCC) and diseases such as Hipbel-Lindau disease, horseshoe
 CC kidneys, adult polycystic kidney disease and acquired renal cystic
 CC disease. FGF-5 polypeptides may be used as immunogen in the production of
 CC antibodies, which are useful in quantitative immunoassays that determine
 CC concentrations of antigen-bearing substances in biological samples, and
 CC to (semi-)quantitatively identify the presence of antigen in a biological
 CC sample. The antibodies may also be used to treat FGF-5 expressing or
 CC overexpressing tumours by decreasing FGF-5 activity, as diagnostic agents
 CC to monitor the progression or regression of an FGF-5 expressing or
 CC overexpressing tumour in a patient undergoing therapy for the treatment
 CC of neoplasm. FGF-5 cDNA is also useful in gene therapy. The present
 CC sequence is a human FGF-5 peptide from clone 6A4-1
 CC
 XX
 SQ Sequence 246 AA;
 Query Match 72.8%; Score 195; DB 4; Length 246;
 Best Local Similarity 100.0%; Pred. No. 2.7e-177;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 EPELSFTVPEKK 237
 |||||
 DB 201 EPELSFTVPEKK 215
 RESULT 14
 AAR70813
 ID AAR70813 standard; protein; 268 AA.
 XX
 AC AAR70813;
 XX
 DT 25-MAR-2003 (revised)
 DT 01-SEP-1995 (first entry)
 XX
 DE FGF-5.
 XX
 KM FGF-5; fibroblast growth factor; cytotoxic conjugate; fusion protein;
 KM saporin; cytostatic; tumor; diabetes; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PA Key Location/Qualifiers
 FT Misc-difference 19 /note= "Cys may be replaced by Ser"
 FT Misc-difference 93 /note= "Cys may be replaced by Ser"
 FT Misc-difference 202 /note= "Cys may be replaced by Ser"
 FT FT Misc-difference /note= "Cys may be replaced by Ser"
 XX
 PN WO9503831-A1.
 XX
 PD 09-FEB-1995.
 XX
 PF 27-JUL-1994; 94WO-US008511.
 XX
 PR 02-AUG-1993; 93US-00099924.
 PR 29-OCT-1993; 93US-00145829.
 XX
 PA (PRIZ-) PRIZM PHARM INC.
 PA (WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
 PI Sosnowski BA, Lappi DA, Baird AJ;
 XX
 DR WPI: 1995-082038/11.
 XX
 CC New monogenous preparations of cytotoxic conjugates and DNA - contain
 CC fibroblast growth factors and cytotoxic agents for treating FGF
 CC PT conditions such as tumours, diabetes and rheumatoid arthritis.
 CC Disclosure; Page 112; 128p; English.
 PS
 XX
 CC Novel fusion proteins comprise FGF linked to saporin. FGF-1 to -9 may be
 CC used, pref. FGF-1 (AAR70812), FGF-5 (AAR70813), FGF-7 (AAR70814) or FGF-8
 CC (AAR70815) muteins, in which at least 1 Cys residue is replaced by
 CC conservative Ser substitutions. The fusion proteins are potent cytotoxic
 CC agents to cells bearing the FGF receptor. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 CC
 XX
 SQ Sequence 268 AA;
 Query Match 72.8%; Score 195; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.9e-177;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 163 RRRFQENSNTYASAIHRTKTKREMYVALNKRGRKAGCCSPRVKQHIISTHFLPRFKQS 222
 QY 223 EQPELSFTYTVPEKK 237
 Db 223 EQPELSFTYTVPEKK 237

RESULT 15

AAR80780
 ID AAR80780 standard; protein; 268 AA.
 XX
 AC AAR80780;

DT 13-MAY-1996 (first entry)
 XX

DE Fibroblast growth factor 5, FGF-5.

XX Conjugate; fibroblast growth factor; FGF; cytotoxin; saporin; eye;
 KW cell proliferation; regulation; pterygia; corneal clouding; cancer;
 KW psoriasis; rheumatoid arthritis.
 XX

OS Homo sapiens.

XX W09524928-A2.

XX 21-SEP-1995.

PF 15-MAR-1995; 95WO-US003448.

XX 15-MAR-1994; 94US-00213446.

PR 15-MAR-1994; 94US-00213447.

XX (PRIZ-) PRIZM PHARM INC.

XX Sosnowski BA, Baird JA, Houston LL, Nova MP;

PI WPI; 1995-136820/43.

DR New conjugates of growth factor receptor ligand and targeted agent -
 PT partic. DNA or cytotoxin, used to control cell proliferation in the eye,
 PT e.g. to prevent growth of pterygia and corneal clouding.

XX Claim 33; Page 144; 204pp; English.

CC AAR80776-84 are fibroblast growth factors (FGF) FGF-1 to FGF-9
 CC respectively. DNA encoding these fibroblast growth factors can be used to
 CC create an FGF/saporin fusion protein. DNA encoding such fusion proteins
 CC are useful for targeting saporin (a cytotoxin) to a cell carrying the
 CC FGF receptor. Targeted agents (TA) other than saporin which may be used
 CC include in partic. DNA encoding a therapeutic protein, antisense DNA or
 CC other cytotoxic agent. The linker sequence within the fusion protein may
 CC increase serum stability or intracellular availability of the TA. The
 CC conjugates of the invention are used to inhibit cell proliferation in
 CC cells carrying the particular growth factor receptor; also when TA is DNA
 CC it can be used to deliver this to cells (for gene therapy). A specific
 CC application is to prevent excessive proliferation of epithelial cells,
 CC fibroblasts and keratinocytes in the anterior eye after surgery, partic.
 CC to prevent recurrence of pterygia after surgical removal, closure of
 CC trabeculectomy after glaucoma surgery and corneal clouding after excimer
 CC laser treatment. Other conditions which may be treated include tumours,
 CC restenosis, psoriasis, Dupuytren's contracture, diabetic complications,
 CC Kaposi's sarcoma and rheumatoid arthritis
 XX

SQ Sequence 268 AA;

Query Match 72.8%; Score 195; DB 2; Length 268;

Best Local Similarity 100.0%; Pred. No. 2,9e-177; Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 43 GSSSRQSSSSAMSSSSAPASLGSQSSGLRQSSFFQWSPSGRTGSLYCRVIGIFHLQ 102

QY 103 IYPDGKNGSHEANMLSVLEIFPAVSGIGVIRGVPSNKFPLAMSKKGLHASAKFTDDCKF 162
 Db 103 IYPDGKNGSHEANMLSVLEIFPAVSGIGVIRGVPSNKFPLAMSKKGLHASAKFTDDCKF 162
 QY 163 RRRFQENSNTYASAIHRTKTKREMYVALNKRGRKAGCCSPRVKQHIISTHFLPRFKQS 222
 Db 163 RRRFQENSNTYASAIHRTKTKREMYVALNKRGRKAGCCSPRVKQHIISTHFLPRFKQS 222
 QY 223 EQPELSFTYTVPEKK 237
 Db 223 EQPELSFTYTVPEKK 237

Search completed: April 11, 2006, 03:33:13
 Job time : 78 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 03:38:41 ; Search time 21 Seconds
(without alignments)
1055.099 Million cell updates/sec

Title: US-10-089-485-18

Perfect score: 268

Sequence: 1 MSLSFLLLPFSHLILSAWA.....LSAPRKNTNSVKYRLKFRFG 268

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	100.0	268	US-09-949-016-7942	Sequence 7942, Ap
2	237	88.4	268	US-09-023-082A-15	Sequence 15, Appl
3	237	88.4	268	US-09-240-952-2	Sequence 2, Appl
4	237	88.4	268	US-09-248-998-15	Sequence 15, Appl
5	237	88.4	268	US-09-610-651-15	Sequence 15, Appl
6	237	88.4	268	US-09-345-373-15	Sequence 15, Appl
7	237	88.4	268	US-10-075-446-15	Sequence 15, Appl
8	216	80.6	248	US-09-240-952-3	Sequence 5, Appl
9	215	80.2	247	US-09-240-952-5	Sequence 5, Appl
10	195	72.8	268	US-08-439-725A-12	Sequence 12, Appl
11	195	72.8	268	US-08-464-590A-17	Sequence 17, Appl
12	195	72.8	268	US-08-207-412B-12	Sequence 12, Appl
13	195	72.8	268	US-08-867-471-12	Sequence 12, Appl
14	195	72.8	268	US-08-438-439C-8	Sequence 8, Appl
15	195	72.8	268	US-08-951-822-33	Sequence 33, Appl
16	195	72.8	268	US-08-718-904-14	Sequence 14, Appl
17	195	72.8	268	US-09-093-585-17	Sequence 17, Appl
18	195	72.8	268	US-09-368-951-33	Sequence 33, Appl
19	195	72.8	268	US-09-449-249-14	Sequence 14, Appl
20	195	72.8	268	US-09-390-207-20	Sequence 20, Appl
21	195	72.8	268	US-09-229-947-33	Sequence 33, Appl
22	195	72.8	268	US-09-572-406B-11	Sequence 11, Appl
23	182	67.9	266	US-09-417-721-9	Sequence 9, Appl
24	172	64.2	219	US-08-441-629-13	Sequence 13, Appl
25	172	64.2	219	US-08-776-207-13	Sequence 13, Appl
26	172	64.2	219	US-09-507-773-13	Sequence 13, Appl
27	172	64.2	219	US-10-016-447-13	Sequence 13, Appl

28	172	64.2	219	4	PCT-US95-09172-13	Sequence 13, Appl
29	156	58.2	266	1	US-08-438-439C-18	Sequence 18, Appl
30	151	56.3	269	2	US-09-417-721-15	Sequence 15, Appl
31	151	56.3	267	1	US-08-462-169B-13	Sequence 13, Appl
32	151	56.3	267	2	US-09-103-079-13	Sequence 13, Appl
33	151	56.3	267	2	US-09-425-021-13	Sequence 13, Appl
34	151	56.3	267	2	US-09-564-829-7	Sequence 7, Appl
35	151	56.3	268	2	US-08-705-245-14	Sequence 14, Appl
36	151	56.3	268	2	US-09-490-714-14	Sequence 14, Appl
37	90	33.6	264	2	US-09-390-207-30	Sequence 30, Appl
38	77	28.7	123	1	US-08-822-573-2	Sequence 2, Appl
39	50	18.7	266	6	5175383-5	Patent No. 5175383
40	39	14.6	121	1	US-08-822-573-4	Sequence 4, Appl
41	27	10.1	27	1	US-08-290-373B-6	Sequence 6, Appl
42	15	5.6	15	2	US-09-537-817B-1	Sequence 1, Appl
43	15	5.6	19	2	US-09-537-817B-10	Sequence 10, Appl
44	13	4.9	13	2	US-09-537-817B-9	Sequence 9, Appl
45	11	4.1	15	2	US-09-537-817B-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-949-016-7942
; Sequence 7942, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7942
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7942
Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-245; Length 268;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MSLSFLLLPFSHLILSAWAHGEKRLAKGPGPAATDRNPRGSSSSSSSSSSSSSSSS 60
1 MSLSFLLLPFSHLILSAWAHGEKRLAKGPGPAATDRNPRGSSSSSSSSSSSSSSSS 60
61 SSPAASLQSGSGLEFQSSFGWSPSGRTGSLYCRVIGIFHLQIYDGVNSHEANMISV 120
61 SSPAASLQSGSGLEFQSSFGWSPSGRTGSLYCRVIGIFHLQIYDGVNSHEANMISV 120
61 SSPAASLQSGSGLEFQSSFGWSPSGRTGSLYCRVIGIFHLQIYDGVNSHEANMISV 120
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121 LEIPVSGIGIVGIRVFNKFLAMSKKGLKLAFAKFTDDCKFRBFQNSVNTVSAIHR 180
121 LEIPVSGIGIVGIRVFNKFLAMSKKGLKLAFAKFTDDCKFRBFQNSVNTVSAIHR 180
181 TEKTRERYVALNKRGAAGCSPRVKQHSITFLPRFQSBQBELSFTVTVPKCKKP 240
181 TEKTRERYVALNKRGAAGCSPRVKQHSITFLPRFQSBQBELSFTVTVPKCKKP 240
241 SPIKXIPLSAPRKNTNSVKYRLKFRFG 268
241 SPIKXIPLSAPRKNTNSVKYRLKFRFG 268
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RESULT 2

US-09-023-082A-15

Sequence 15, Application US/09023082A

Patent No. 6077682

GENERAL INFORMATION:

APPLICANT: ROSEN, STEVEN M.

APPLICANT: JIMENEZ, PABLO

APPLICANT: DUAN, D. ROXANNE

APPLICANT: RAMPE, MARK A.

APPLICANT: MENDRICK, DONNA

APPLICANT: ZHANG, JUN

APPLICANT: NI, JIAN

APPLICANT: MOORE, PAUL A.

APPLICANT: COLEMAN, TIMOTHY A.

APPLICANT: GRUBER, JOACHIM R.

APPLICANT: DILLON, PATRICK J.

TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 NEW YORK AVE, NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,082A

FILING DATE: 13-FEB-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01790

FILING DATE: 14-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/461,195

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/023,852

FILING DATE: 13-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/039,045

FILING DATE: 28-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/862,432

FILING DATE: 23-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/910,875

FILING DATE: 13-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/055,561

FILING DATE: 13-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: STEFFER, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0360008/EKS

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLSCUPE TYPE: protein

US-09-023-082A-15

Query Match

Best Local Similarity 100.0%; Pred. No. 5.6e-216;

Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFFSHLLISAMHAGEKRLAPKGPATDRNRGSSSRSSSAMSSSAS 60

DB 1 MSLSFLLLFFSHLLISAMHAGEKRLAPKGPATDRNRGSSSRSSSAMSSSAS 60

QY 61 SSPASLGSQSGSGLEQSSFGWSPSGRTGSLYCRVGIFGFIQIYDGVKNSGHEANMLSV 120

DB 61 SSPASLGSQSGSGLEQSSFGWSPSGRTGSLYCRVGIFGFIQIYDGVKNSGHEANMLSV 120

QY 121 LEIFAVSQGIIVGIRGVFNKFLAMSKKGLASAKFTDDCKFRERFQENSNTYASAIHR 180

DB 121 LEIFAVSQGIIVGIRGVFNKFLAMSKKGLASAKFTDDCKFRERFQENSNTYASAIHR 180

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

QY 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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DB 181 TKTGREWYVALNKGKAKGCSPPVQPHSTHPLRFKSGEDELSTVTYPERK 237

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Db      61 SSPASISQSGGLEQSSFGWSPSGRRTGSLYCRVIGIHFHLQIYDPGKVNCSHEANMLSV 120
Qy      121 LEIFAVSGIIVGIRVFNKFLAMSKKGLHASAKFTDDCKRFRFOENSYNTYASAIHR 180
Db      121 LEIFAVSGIIVGIRVFNKFLAMSKKGLHASAKFTDDCKRFRFOENSYNTYASAIHR 180
Qy      181 TEKTRERNYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEBELSFTYVPEKK 237
Db      181 TEKTRERNYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEBELSFTYVPEKK 237

RESULT 4
US-09-248-998-15
; Sequence 15, Application US/09248998
; Patent No. 6599879
; GENERAL INFORMATION:
; APPLICANT: Jimenez, Pablo
; APPLICANT: Rampey, Mark A.
; APPLICANT: Mendrick, Donna
; APPLICANT: Ruseell, Deborah
; APPLICANT: Louie, Arthur
; TITLE OF INVENTION: Therapeutic Uses of Keratinocyte Growth Factor-2
; FILE REFERENCE: 1488.1060002
; CURRENT APPLICATION NUMBER: US/09/248,998
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: US 60/114,387
; EARLIER FILING DATE: 30-DEC-1998
; EARLIER APPLICATION NUMBER: US 60/074,585
; EARLIER FILING DATE: 13-FEB-1998
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-248-998-15

Query Match      88.4%; Score 237; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.6e-216;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSLSLILLFSSHLLISAMAHGEKRLAPKGPAPATDRNPRGSSSSROSSSAMSSSSAS 60
Db      1 MSLSLILLFSSHLLISAMAHGEKRLAPKGPAPATDRNPRGSSSSROSSSAMSSSSAS 60
Qy      61 SSPASISQSGGLEQSSFGWSPSGRRTGSLYCRVIGIHFHLQIYDPGKVNCSHEANMLSV 120
Db      61 SSPASISQSGGLEQSSFGWSPSGRRTGSLYCRVIGIHFHLQIYDPGKVNCSHEANMLSV 120
Qy      121 LEIFAVSGIIVGIRVFNKFLAMSKKGLHASAKFTDDCKRFRFOENSYNTYASAIHR 180
Db      121 LEIFAVSGIIVGIRVFNKFLAMSKKGLHASAKFTDDCKRFRFOENSYNTYASAIHR 180
Qy      181 TEKTRERNYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEBELSFTYVPEKK 237
Db      181 TEKTRERNYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEBELSFTYVPEKK 237

RESULT 5
US-09-610-651-15
; Sequence 15, Application US/09610651
; Patent No. 6693077
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jimenez, Pablo
; APPLICANT: Duan, D. Roxanne
; APPLICANT: Rampey, Mark A.
; APPLICANT: Mendrick, Donna
; APPLICANT: Zhang, Jun
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul A.
; APPLICANT: Coleman, Timothy A.
; APPLICANT: Gruber, Joachim R.
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; APPLICANT: Dillon, Patrick J.
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2
; FILE REFERENCE: 1488.0360007
; CURRENT APPLICATION NUMBER: US/09/610,651
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: PCT/US95/01790
; PRIOR FILING DATE: 1995-02-14
; PRIOR APPLICATION NUMBER: 08/461,195
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/696,135
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 08/862,432
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/023,852
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 60/039,045
; PRIOR FILING DATE: 1997-02-28
; PRIOR APPLICATION NUMBER: 60/055,561
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 08/910,875
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/023,082
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/345,373
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/142,343
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/143,648
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/144,024
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/148,628
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/149,935
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/163,375
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: 60/171,677
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/205,417
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/198,322
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-610-651-15

Query Match      88.4%; Score 237; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.6e-216;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSLSLILLFSSHLLISAMAHGEKRLAPKGPAPATDRNPRGSSSSROSSSAMSSSSAS 60
Db      1 MSLSLILLFSSHLLISAMAHGEKRLAPKGPAPATDRNPRGSSSSROSSSAMSSSSAS 60
Qy      61 SSPASISQSGGLEQSSFGWSPSGRRTGSLYCRVIGIHFHLQIYDPGKVNCSHEANMLSV 120
Db      61 SSPASISQSGGLEQSSFGWSPSGRRTGSLYCRVIGIHFHLQIYDPGKVNCSHEANMLSV 120
Qy      121 LEIFAVSGIIVGIRVFNKFLAMSKKGLHASAKFTDDCKRFRFOENSYNTYASAIHR 180
Db      121 LEIFAVSGIIVGIRVFNKFLAMSKKGLHASAKFTDDCKRFRFOENSYNTYASAIHR 180
Qy      181 TEKTRERNYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEBELSFTYVPEKK 237
Db      181 TEKTRERNYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEBELSFTYVPEKK 237
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RESULT 6
US-09-345-373-15
Sequence 15, Application US/09345373
Patent No. 6903072
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RAMPEY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,373
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: No. 6903072 Relevantant
TOPOLOGY: No. 6903072 Relevantant
MOLECULE TYPE: Protein
US-09-345-373-15

Query Match 88.4%; Score 237; DB 2; Length 268;

Best Local Similarity 100.0%; Pred. No. 5.6e-216;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLLPFSHILTSAMAGEKRLAPGPGPAATRNRRGSSSSRQSSSAMSSSSAS 60
DB 1 MSLSFLLLPFSHILTSAMAGEKRLAPGPGPAATRNRRGSSSSRQSSSAMSSSSAS 60
QY 61 SSPASLSGSGSGLEQSSFSQSPSGRRTGSLYCRVIGIFHLQIYDPGVNCSHEANMLSV 120
DB 61 SSPASLSGSGSGLEQSSFSQSPSGRRTGSLYCRVIGIFHLQIYDPGVNCSHEANMLSV 120
QY 121 LEIFAVSGIYVIGIRVFNKFLAMSKKGLHSAKFTDCKFRERFQENSTVTYSAIHR 180
DB 121 LEIFAVSGIYVIGIRVFNKFLAMSKKGLHSAKFTDCKFRERFQENSTVTYSAIHR 180
QY 181 TEKGRWYVALNKRKAKRGCSPPVKKQHTSTHLPFRFKOSEOPELSFTVTVPKK 237
DB 181 TEKGRWYVALNKRKAKRGCSPPVKKQHTSTHLPFRFKOSEOPELSFTVTVPKK 237
RESULT 7
US-10-075-446-15
Sequence 15, Application US/10075446
Patent No. 6916786
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RAMPEY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/075,446
FILING DATE: 15-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688

? RESEQUENCE/DOCKET NUMBER: 1488.0360008/EKSK
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 202-371-2600
 ? TELEFAX: 202-371-2540
 ? INFORMATION FOR SEQ ID NO: 15:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 268 amino acids
 ? TYPE: amino acid
 ? STANDEDNESS: No. 6916786 Relevant
 ? TOPOLOGY: No. 6916786 Relevant
 ? MOLECULE TYPE: protein
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 ? US-10-075-446-15

Query Match	88.4%	Score 237	DB 2	Length 268
Best Local Similarity	100.0%	Pred. No	5.6e-216	
Matches 237	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Db	1	MSLSLTLTLTLFFSHLILISAHAHGKRLAPKQOPPAATDTRNRPSSSSSSSSAMSSSSAS	60
Qy	61	SSPAASLGSQSGGLEQSSSFQWSPSPSGRTGSLYRGVIGFHLQIYPDGKVNGSHEANLSTV	120
Db	61	SSPAASLGSQSGGLEQSSSFQWSPSPSGRTGSLYRGVIGFHLQIYPDGKVNGSHEANLSTV	120
Qy	121	LEIFAVSQGIVIGIRGVFSNKPFLAMSKKGLKHLASAKTTDDCKFPERFOENSINTYASAIHR	180
Db	121	LEIFAVSQGIVIGIRGVFSNKPFLAMSKKGLKHLASAKTTDDCKFPERFOENSINTYASAIHR	180
Qy	181	TEKTRREMYVALNKKGKAKRGCSPRYKPHIISTHFLPRFQSGROPELSFTVYVPEKK	237
Db	181	TEKTRREMYVALNKKGKAKRGCSPRYKPHIISTHFLPRFQSGROPELSFTVYVPEKK	237

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; LENGTH: 248 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-240-952-3

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Query Match	80.6%	Score 216;	DB 2;	Length 248;
Best Local Similarity	100.0%	Pred. No. 3.8e-196;		
Matches 216; Conservative	0;	Mismatches	0;	Gaps 0;

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Dd	2	GERRLAPKQOPGPAATDRNPRGSSSRQSSSSAMSSSSASPPASLSQSGGLEQSSFFOW	61
Qy	82	SPSGRRTGSILYCRVGIQPHLOIYDPGKYNCSHEANMLSVLEIFAVSOGIVGIRGVFSNKP	141
Dd	62	SPSGRRTGSILYCRVGIQPHLOIYDPGKYNCSHEANMLSVLEIFAVSOGIVGIRGVFSNKP	121
Qy	142	LMSKKGGKHAASAKPFDDCFKPRERQENSNTYTYASALHRTKTKGREWYVALNRGKAKRG	201
Dd	122	LMSKKGGKHAASAKPFDDCFKPRERQENSNTYTYASALHRTKTKGREWYVALNRGKAKRG	181
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Dd	182	CSPRVAKPOHISTHFLPRFKQSEOPSLSTVTVVPEKK	217

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1      RESULT 9
2      US-09-240-952-5
3      Sequence 5, Application US/09240952
4      Patent No. 6331523
5      GENERAL INFORMATION:
6      APPLICANT: Kijavin, Ivar
7      APPLICANT: La Fleur, Monique
8      TITLE OF INVENTION: Method of Preventing the Death of Retinal
9      TITLE OF INVENTION: Neurons and Treating Ocular Diseases
10     NUMBER OF SEQUENCES: 5
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Genentech, Inc.
13     STREET: 1 DNA Way
14     CITY: South San Francisco
15     STATE: California
16     COUNTRY: USA
17     ZIP: 94080
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: WinPatIn (Genentech)
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/09/240,952
25     FILING DATE: 29-Jan-1999
26     CLASSIFICATION:
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER: 09/041,383
29     FILING DATE: 12-Mar-98
30     ATTORNEY/AGENT INFORMATION:
31     NAME: Svoboda, Craig G.
32     REGISTRATION NUMBER: 39,044
33     REFERENCE/DOCKET NUMBER: P1088P1
34     TELECOMMUNICATION INFORMATION:
35     TELEPHONE: 650/225-1489
36     TELEFAX: 650/952-9881
37     INFORMATION FOR SEQ ID NO: 5:
38     SEQUENCE CHARACTERISTICS:
39     LENGTH: 247 amino acids
40     TYPE: amino acid
41     TOPOLOGY: Linear
42     US-09-240-952-5
43
44     Query Match      80.2%; Score 215; DB 2; Length 247;
45     Best Local Similarity 100.0%; Freq. No. 3.3e-195;
46     Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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1 STREET 4225 Executive Square, Suite 1400
2 CITY: La Jolla
3 STATE: CA
4 COUNTRY: USA
5 ZIP: 92037
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patentln Release #1.0, Version #1.30
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/867,471
14 FILING DATE: 02-JUN-1997
15 CLASSIFICATION: 536
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/439,725
18 FILING DATE: 12-MAY-1995
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Haile, Lisa A.
21 REGISTRATION NUMBER: 38,347
22 REFERENCE/DOCKET NUMBER: 07265/047001
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 619/678-5070
25 TELEFAX: 617/678-5099
26 INFORMATION FOR SEQ ID NO: 12:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 268 amino acids
29 TYPE: amino acid
30 STRANDEDNESS: not relevant
31 TOPOLOGY: linear
32 MOLECULE TYPE: protein
33
34 US-08-867-471-12
35
36 Query Match 72.8%; Score 195; DB 1; Length 268;
37 Best Local Similarity 100.0%; Pred. No. 2,9e-176;
38 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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41 43 GSSSRQSSSSAMSSSSASSPASISQSGSGLEQSSFWQSPSGRTSLYCRVIGIFHLQ 102
42 Db
43 103 IYPPGKXNGSHKAMLSYLFPAVSQGIYGRVPSNKPFLAMSKKGLHSAKFTDCKP 162
44 103 IYPPGKXNGSHKAMLSYLFPAVSQGIYGRVPSNKPFLAMSKKGLHSAKFTDCKP 162
45 QY 163 RERPOENSYNFYASAIHRTKTXGKEMVYALNKGKAKRGCSPRVYKPOHISTHPLPRFKOS 222
46 163 RERQENSINTFYASAIHRTKTXGKEMVYALNKGKAKRGCSPRVYKPOHISTHPLPRFKOS 222
47 Db
48 223 EQPELSFTVTVPEKK 237
49 223 EQPELSFTVTVPEKK 237
50 QY
51 223 EQPELSFTVTVPEKK 237
52 223 EQPELSFTVTVPEKK 237
53 Db
54 223 EQPELSFTVTVPEKK 237
55 223 EQPELSFTVTVPEKK 237
56
57 RESULT 14
58 US-08-438-439C-8
59 ; Sequence 8, Application US/08438439C
60 ; Patent No. 5876967
61 ;
62 GENERAL INFORMATION:
63 APPLICANT: Nathan, Jeremy
64 APPLICANT: Smallwood, Phillip M.
65 APPLICANT: Macke, Jennifer P.
66 TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
67 TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
68 NUMBER OF SEQUENCES: 25
69 CORRESPONDENCE ADDRESS:
70 ADDRESSEE: Fish & Richardson P.C.
71 STREET: 4225 Executive Square, Suite 1400
72 CITY: La Jolla
73 STATE: CA
74 COUNTRY: USA
75 ZIP: 92037
76
77 COMPUTER READABLE FORM:

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1      MEDIUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: PatentIn Release #1.0, Version #1.30
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/08/438,439C
7      FILING DATE: May 12, 1995
8      CLASSIFICATION: 435
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Haile, Lisa A.
11     REGISTRATION NUMBER: 38,347
12     REFERENCE/DOCKET NUMBER: 07265/046001
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: 619/678-5070
15     TELEFAX: 619/678-5099
16     INFORMATION FOR SEQ ID NO: 8:
17     SEQUENCE CHARACTERISTICS:
18     LENGTH: 268 amino acids
19     TYPE: amino acid
20     STRANDEDNESS: not relevant
21     TOPOLOGY: linear
22     MOLECULE TYPE: protein
23     US-08-438-439C-8

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Query Match	72.8%	Score 195;	DB 1;	Length 268;
Best Local Similarity	100.0%	Pred. No. 2.9e-176;		
Matches 195;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Qy	103	YYPDGKVGSGHEANMLSVLEIFAVSGIGVIRGVFSPNKFLLAMSKKGLHASAKFTDDCKF	162
Db	103	YYPDGKVGSGHEANMLSVLEIFAVSGIGVIRGVFSPNKFLLAMSKKGLHASAKFTDDCKF	162
Qy	163	RRFQENSINYNTYASAIHRTEKTGREYVALNTRGKAKRGCSPRVKQHIISTHFLPRPKOS	222
Db	163	RRFQENSINYNTYASAIHRTEKTGREYVALNTRGKAKRGCSPRVKQHIISTHFLPRPKOS	222
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RESULT 15
US-08-951-822-33

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Sequence 33, Application US/08951822A
Patent No. 5989866
GENERAL INFORMATION:
APPLICANT: Deliber, Theresa A.
APPLICANT: Conklin, Darrell C.
APPLICANT: Raymond, Fenella
APPLICANT: Bukowski, Thomas R.
APPLICANT: Holderman, Susan D.
APPLICANT: Hansen, Birgit
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGR HOMOLOGS
FILE REFERENCE: 96-20
CURRENT APPLICATION NUMBER: US/08/951,822A
CURRENT FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 266
TYPE: prt
ORGANISM: Homo sapiens
US-08-951-822-33

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Query Match	72.8%;	Score 195;	DB 1;	Length 268;
Best Local Similarity	100.0%;	Pred. No. 2.9e-176;		
Matches 195;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Job time : 22 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 03:43:16 ; Search time 60.5 Seconds
(without alignments)
1850.880 Million cell updates/sec

Title: US-10-089-485-18

Perfect score: 268

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Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 1

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	237	88.4	268	3	US-09-345-373-15 Sequence 15, Appl
2	237	88.4	268	4	US-10-075-446-15 Sequence 15, Appl
3	237	88.4	268	4	US-10-035-212-15 Sequence 15, Appl
4	237	88.4	268	5	US-10-733-311-15 Sequence 15, Appl
5	237	88.4	268	5	US-10-868-577A-27 Sequence 27, Appl
6	237	88.4	268	5	US-10-901-210-15 Sequence 15, Appl
7	195	72.8	268	3	US-09-284-663A-10 Sequence 10, Appl
8	195	72.8	268	3	US-09-750-963-11 Sequence 11, Appl
9	195	72.8	268	3	US-09-502-773A-7 Sequence 7, Appl
10	195	72.8	268	3	US-09-251-263-12 Sequence 12, Appl
11	195	72.8	268	4	US-10-081-347-33 Sequence 33, Appl
12	195	72.8	268	4	US-10-189-360-14 Sequence 14, Appl
13	195	72.8	268	4	US-10-192-988-8 Sequence 8, Appl
14	195	72.8	268	4	US-10-315-431-33 Sequence 33, Appl
15	195	72.8	268	4	US-10-347-177-11 Sequence 11, Appl
16	195	72.8	268	4	US-10-372-653-11 Sequence 11, Appl
17	195	72.8	268	4	US-10-037-922-33 Sequence 33, Appl
18	195	72.8	268	5	US-10-854-485-33 Sequence 33, Appl
19	195	72.8	268	5	US-10-413-537-10 Sequence 10, Appl
20	182	67.9	268	4	US-10-131-965-9 Sequence 9, Appl
21	172	64.2	219	4	US-10-016-447-13 Sequence 13, Appl
22	156	58.2	269	4	US-10-192-988-18 Sequence 18, Appl
23	151	56.3	247	4	US-10-023-592-9 Sequence 9, Appl
24	151	56.3	266	4	US-10-131-965-15 Sequence 15, Appl
25	151	56.3	267	3	US-09-822-485-8 Sequence 8, Appl
26	151	56.3	267	3	US-09-425-021-13 Sequence 13, Appl
27	151	56.3	267	4	US-10-023-592-7 Sequence 7, Appl

28	151	56.3	267	4	US-10-374-207-8 Sequence 8, Appl
29	151	56.3	267	4	US-10-123-481-7 Sequence 7, Appl
30	151	56.3	267	5	US-10-935-226-7 Sequence 7, Appl
31	151	56.3	267	5	US-10-932-284-7 Sequence 7, Appl
32	151	56.3	267	5	US-10-690-019-14 Sequence 14, Appl
33	144	53.7	268	4	US-09-901-938-27 Sequence 27, Appl
34	144	53.7	144	4	US-10-379-334-27 Sequence 27, Appl
35	82	30.6	82	3	US-09-801-968-39 Sequence 39, Appl
36	82	30.6	82	3	US-09-802-154-39 Sequence 39, Appl
37	11	4.1	173	4	US-10-767-701-41558 Sequence 41558, A
38	11	4.1	287	4	US-10-425-114-59971 Sequence 59971, A
39	10	3.7	10	3	US-09-572-404B-3798 Sequence 3798, Ap
40	10	3.7	10	3	US-09-572-404B-3799 Sequence 3799, Ap
41	10	3.7	109	4	US-10-451-467A-282 Sequence 282, App
42	10	3.7	359	4	US-10-437-963-187082 Sequence 187082, A
43	10	3.7	502	6	US-11-097-143-23466 Sequence 23466, A
44	9	3.4	9	4	US-10-424-955A-36 Sequence 36, Appl
45	9	3.4	9	5	US-10-982-514-37 Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-345-373-15
; Sequence 15, Application US/09345373
; Publication No. US2003077695A1
; GENERAL INFORMATION:
; APPLICANT: RUBEN, STEVEN M.
; APPLICANT: JIMENEZ, PABLO
; APPLICANT: DUAN, D. ROXANNE
; APPLICANT: RAMPY, MARK A.
; APPLICANT: MENDRICK, DONNA
; APPLICANT: ZHANG, JUN
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL A.
; APPLICANT: COLEMAN, TIMOTHY A.
; APPLICANT: GRUBER, JOACHIM R.
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: GENTZ, REINER L.
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,373
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,195
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,852
; FILING DATE: 13-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,045
; FILING DATE: 28-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,432
; FILING DATE: 23-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFER, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030077695A1 Relevant
TOPOLOGY: No. US20030077695A1 Relevant
MOLECULE TYPE: protein
US-09-345-373-15

Query Match 88.4%; Score 237; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSLSFLILFFSHLILSAMHGEKRLAPKQGPATDNRPGSSSSSSSSSSSSSSSS 60
QY 61 SSPASISGSGGLEQSSPQWSPSGRRTGSLYCRVIGIHFHQLIYPDGKNGSHEANMLSV 120
DB 61 SSPASISGSGGLEQSSPQWSPSGRRTGSLYCRVIGIHFHQLIYPDGKNGSHEANMLSV 120
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DB 121 LEIFAVSOGIVIGIRGVFSNKFPLAMSKGKGLHSAKFTDDCKRERFOENSNTYTSAIRH 180
QY 181 TKTGREWYVALNKGKAKRGCSPRVKPQHISTHFLPRFKOSEPBLSTVTVPPEKK 237
DB 181 TKTGREWYVALNKGKAKRGCSPRVKPQHISTHFLPRFKOSEPBLSTVTVPPEKK 237

RESULT 2
US-10-075-446-15

Sequence 15, Application US/10075446
Publication No. US20030129687A1
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.

JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK A.
MENDRICK, DONNA
ZHANG, JUN
NI, JIAN
MOORE, PAUL A.
COLEMAN, TIMOTHY A.

GRUBER, JOACHIM R.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON

STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/075,446
FILING DATE: 15-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE: <Unknown>

APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/910,875
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: 1488.0360008/EKS
ATTORNEY/AGENT INFORMATION:
NAME: STEFFER, ERIC K.

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030129687A1 Relevant
TOPOLOGY: No. US20030129687A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-075-446-15

Query Match 88.4%; Score 237; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SSPASISGSGGLEQSSPQWSPSGRRTGSLYCRVIGIHFHQLIYPDGKNGSHEANMLSV 120
QY 121 LEIFAVSOGIVIGIRGVFSNKFPLAMSKGKGLHSAKFTDDCKRERFOENSNTYTSAIRH 180
DB 121 LEIFAVSOGIVIGIRGVFSNKFPLAMSKGKGLHSAKFTDDCKRERFOENSNTYTSAIRH 180
QY 181 TKTGREWYVALNKGKAKRGCSPRVKPQHISTHFLPRFKOSEPBLSTVTVPPEKK 237
DB 181 TKTGREWYVALNKGKAKRGCSPRVKPQHISTHFLPRFKOSEPBLSTVTVPPEKK 237

RESULT 3
US-10-035-212-15

Sequence 15, Application US/10035212
Publication No. US20030186904A1
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.

JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK A.
MENDRICK, DONNA
ZHANG, JUN
NI, JIAN
MOORE, PAUL A.
COLEMAN, TIMOTHY A.

GRUBER, JOACHIM R.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICANT: Dillon, Patrick J.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Keratinocyte Growth Factor-2
FILE REFERENCE: 1488.0360000
CURRENT APPLICATION NUMBER: US/10/035,212
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/286,368
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/331,168
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-10-035-212-15

Query Match 88.4%; Score 237; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-733-311-15

Sequence 15, Application US/10733311
Publication No. US20040224387A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
APPLICANT: Jimenez, Pablo
APPLICANT: Duan, D. Roxanne
APPLICANT: Rampy, Mark A.
APPLICANT: Mendrick, Donna
APPLICANT: Zhang, Jun
APPLICANT: Ni, Jian
APPLICANT: Moore, Paul A.
APPLICANT: Coleman, Timothy A.
APPLICANT: Gruber, Joachim R.
APPLICANT: Dillon, Patrick J.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Keratinocyte Growth Factor-2
FILE REFERENCE: 1488.036000J
CURRENT APPLICATION NUMBER: US/10/733,311
CURRENT FILING DATE: 2003-12-12
PRIOR APPLICATION NUMBER: US/09/610,651
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: PCT/US95/01790
PRIOR FILING DATE: 1995-02-14
PRIOR APPLICATION NUMBER: 08/461,195
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 08/696,135
PRIOR FILING DATE: 1996-08-13
PRIOR APPLICATION NUMBER: 08/862,432
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/023,852

PRIOR FILING DATE: 1996-08-13
PRIOR APPLICATION NUMBER: 60/039,045
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: 60/055,561
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 08/910,875
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 09/023,082
PRIOR FILING DATE: 1998-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-10-733-311-15

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Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SSPAASLGSQSGLEQSSFFOWSPSGRRGSLYCRVIGIFHLQIYPDGKNSHEANMLSV 120
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DB 181 TEKGRBMYVALNKGKAKRGCSPRVKPOHISTHFLPRFKOSEBELSFTYVPEKK 237

RESULT 5
US-10-868-577A-27

Sequence 27, Application US/10868577A
Publication No. US20050032697A1
GENERAL INFORMATION:
APPLICANT: Alitalo et al.
TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
FILE REFERENCE: 28967/39359A
CURRENT APPLICATION NUMBER: US/10/868,577A
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US 60/478,390
PRIOR FILING DATE: 2003-06-12
PRIOR APPLICATION NUMBER: US 10/669,176
PRIOR FILING DATE: 2003-09-23
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-10-868-577A-27

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Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 TEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOSEQPELSFTVTVPBEKK 237
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RESULT 6
US-10-901-210-15
; Sequence 15, Application US/10901210
; Publication No. US20050037966A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2
; FILE REFERENCE: PF15P2D1
; CURRENT APPLICATION NUMBER: US/10/901,210
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 10/035,212
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,853
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/286,368
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/331,168
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-210-15

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Db 121 LEIFAVSOGIVGIRGVSNKFLAMSKKGLHASAKFTDDCKRFRFOENSNTYTAIAHR 180
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Qy 181 TEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOSEQPELSFTVTVPBEKK 237
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RESULT 7
US-09-284-663A-10
; Sequence 10, Application US/09284663A
; Patent No. US20020012961A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Roy, Margaret Ann
; TITLE OF INVENTION: Fibroblast Growth Factor-19
; FILE REFERENCE: P1219R1(e)
; CURRENT APPLICATION NUMBER: US/09/284,663A
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 10
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; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-663A-10

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Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 103 IYPDGKNGSHEANMLSVLEIFAVSOGIVGIRGVSNKFLAMSKKGLHASAKFTDDCKF 162
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Db 103 IYPDGKNGSHEANMLSVLEIFAVSOGIVGIRGVSNKFLAMSKKGLHASAKFTDDCKF 162
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Db 163 RERFOENSNTYTAIAIHRTEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOS 222
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Qy 223 EQPELSFTVTVPBEKK 237
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Db 223 EQPELSFTVTVPBEKK 237
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RESULT 8
US-09-750-963-11
; Sequence 11, Application US/09750963
; Patent No. US20020031805A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGP10
; FILE REFERENCE: 99-83
; CURRENT APPLICATION NUMBER: US/09/750,963
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,578
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-750-963-11

Query Match 72.8%; Score 195; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.7e-171;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 163 RERFOENSNTYTAIAIHRTEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOS 222
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Db 163 RERFOENSNTYTAIAIHRTEKTRGEMVVALNKRKGAKRGCSPRVKPOHISTHFLPRFKOS 222
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Qy 223 EQPELSFTVTVPBEKK 237
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Db 223 EQPELSFTVTVPBEKK 237
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RESULT 9
US-09-902-773A-7
; Sequence 7, Application US/09902773A
; Patent No. US20020034787A1
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
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EARLIER APPLICATION NUMBER: 08/867, 471
EARLIER FILING DATE: 1997-06-02
EARLIER APPLICATION NUMBER: 08/439, 725
EARLIER FILING DATE: 1995-05-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-09-251-263-12

Query Match
Best Local Similarity 100.0%; Pred. NO. 2.7e-171;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DB 163 REFPGNSNTYASAIHRTKGTGBWYVALNKRKARGCSPRVKPQHISTHFLPRPKOS 222
QY 223 EPELSFTYVPEKK 237
DB 223 EPELSFTYVPEKK 237

RESULT 11
US-10-081-347-33
Sequence 33, Application US/10081347
Publication No. US20030008351A1
GENERAL INFORMATION:
APPLICANT: Delisher, Theresa A.
APPLICANT: Conklin, Darrell C.
APPLICANT: Raymond, Penella
APPLICANT: Bukowski, Thomas R.
APPLICANT: Holdeman, Susan D.
APPLICANT: Hansen, Birgit
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFERENCE: 96-20C1
CURRENT APPLICATION NUMBER: US/10/081,347
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US/09/229,947
PRIOR FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-10-081-347-33

Query Match
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DB 223 EPELSFTYVPEKK 237

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Db 163 RRFQENSNTYASAIHRTKTEGREMYVALNKGKAKGCSPRVVKQHI1STHFLPRFKOS 222
QY 223 EQPELSFTVTVEBKK 237
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RESULT 12
US-10-189-360-14
; Sequence 14, Application US/10189360
; Publication No. US20030143217A1
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS
; FOR THERAPE
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/189,360
; FILING DATE: 02-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030143217A1Leuburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.415C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
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; STRANDEDNESS: single
; TOPOLOGY: unknown
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; FEATURE:
; OTHER INFORMATION: /note= "FGF-5"
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Db 163 RRFQENSNTYASAIHRTKTEGREMYVALNKGKAKGCSPRVVKQHI1STHFLPRFKOS 222
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Db 223 EQPELSFTVTVEBKK 237

RESULT 13
US-10-192-988-8
; Sequence 8, Application US/10192988
; Publication No. US20030166875A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: NATHANS, Jeremy
; APPLICANT: SMALLWOOD, Philip M.
; APPLICANT: MACKIE, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR-2 AND METHODS OF USE
; FILE REFERENCE: JHU1230-2
; CURRENT APPLICATION NUMBER: US/10/192,988
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 09/261,007
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/438,439
; PRIOR FILING DATE: 1995-05-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Mammalian
US-10-192-988-8

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Best Local Similarity 100.0%; Pred. No. 2.7e-171;
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RESULT 14
US-10-315-431-33
; Sequence 33, Application US/10315431
; Publication No. US2003019943A1
; GENERAL INFORMATION:
; APPLICANT: Ellsworth, Jeff L.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Moore, Emma E.
; APPLICANT: Wahl, Alan F.
; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
; FILE REFERENCE: 96-20C4
; CURRENT APPLICATION NUMBER: US/10/315,431
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/634,318
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 268
; TYPE: PRT

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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Title: US-10-089-485-18

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	195	72.8	268	7	US-11-134-703-4
5	182	67.9	266	7	US-11-238-936-9
6	176	65.7	176	7	US-11-134-703-8
7	151	56.3	266	7	US-11-238-936-15
8	145	54.1	176	7	US-11-134-703-6
9	60	22.4	60	7	US-11-134-703-19
10	52	19.4	52	7	US-11-134-703-37
11	49	18.3	49	7	US-11-134-703-38
12	48	17.9	48	7	US-11-134-703-36
13	10	3.7	10	7	US-11-134-703-32
14	9	3.4	188	7	US-11-087-099-8568
15	9	3.4	413	7	US-11-096-568A-20771
16	9	3.4	446	6	US-10-714-887-214
17	8	3.0	10	7	US-11-134-703-33
18	8	3.0	153	7	US-11-096-568A-5443
19	8	3.0	202	6	US-10-793-625-1108
20	8	3.0	205	7	US-11-238-936-8
21	8	3.0	207	7	US-11-238-936-10
22	8	3.0	333	7	US-11-096-568A-26084
23	8	3.0	384	7	US-11-096-568A-33509
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26	8	3.0	791	6	US-10-821-234-962	Sequence 962, App
27	8	3.0	3969	6	US-10-974-127A-59	Sequence 59, Appl
28	7	2.6	25	7	US-11-058-735-61	Sequence 61, Appl
29	7	2.6	54	7	US-11-150-054A-34	Sequence 34, Appl
30	7	2.6	98	6	US-10-510-386-138	Sequence 138, App
31	7	2.6	110	7	US-11-072-512-3422	Sequence 3422, App
32	7	2.6	112	7	US-11-096-568A-7612	Sequence 7612, App
33	7	2.6	115	7	US-11-004-399-2629	Sequence 2629, App
34	7	2.6	133	6	US-10-523-362-22	Sequence 22, Appl
35	7	2.6	141	7	US-11-096-568A-13393	Sequence 13393, A
36	7	2.6	163	7	US-11-172-740-2378	Sequence 2378, App
37	7	2.6	164	7	US-11-207-847-4	Sequence 4, Appl1
38	7	2.6	176	7	US-11-096-568A-7838	Sequence 7838, App
39	7	2.6	180	7	US-11-096-568A-12758	Sequence 12758, A
40	7	2.6	186	7	US-11-044-899-21	Sequence 21, Appl
41	7	2.6	186	7	US-11-044-899-22	Sequence 22, Appl
42	7	2.6	186	7	US-11-096-568A-17455	Sequence 17455, A
43	7	2.6	191	6	US-10-991-285-873	Sequence 873, App
44	7	2.6	193	7	US-11-238-936-11	Sequence 11, Appl
45	7	2.6	198	7	US-11-096-568A-18593	Sequence 18593, A

ALIGNMENTS

RESULT 1
US-11-134-703-18
; Sequence 18, Application US/11134703
; Publication No. US2006009393A1
; GENERAL INFORMATION:
; APPLICANT: Hanada et al.
; TITLE OR INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427,920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089,485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-703-18

Query Match 100.0%; Score 268; DB 7; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.1e-246; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0;

QY	1	MSLSFLILFFSHLILSAMAAGEKRLAPQGPAPATDRNPRGSSSSSSSSSSSSSSSS	60
DB	1	MSLSFLILFFSHLILSAMAAGEKRLAPQGPAPATDRNPRGSSSSSSSSSSSSSSSS	60
QY	61	SSPAAISLQSGSGLEQSSFPWSPSGRRRTGSLYCRVGIFPHLIQIYDGKYNSHENMTLSV	120
DB	61	SSPAAISLQSGSGLEQSSFPWSPSGRRRTGSLYCRVGIFPHLIQIYDGKYNSHENMTLSV	120
QY	121	LEIFAVSGIYIGIRGVFNKFLAMSKKGLTASAKFTDDCKPRFRFQENSVYTVASATHR	180
DB	121	LEIFAVSGIYIGIRGVFNKFLAMSKKGLTASAKFTDDCKPRFRFQENSVYTVASATHR	180
QY	181	TEKTRREMYVVALNKRKAKRGCSPPVQDHISTHFLPRFKOSBOBELSFYTVPEKKPP	240
DB	181	TEKTRREMYVVALNKRKAKRGCSPPVQDHISTHFLPRFKOSBOBELSFYTVPEKKPP	240

QY 163 RRRPQNSYNTYASAIHRTKTKGREMYVALNKRGAKKGCSPRVKKPQHISTHLPKFKOS 222
| | | | |
Db 163 RRRPQNSYNTYASAIHRTKTKGREMYVALNKRGAKKGCSPRVKKPQHISTHLPKFKOS 222
QY 223 EQPESLFTVTVPEKK 237
| | | | |
Db 223 EQPESLFTVTVPEKK 237
RESULT 5
US-11-238-936-9
; Sequence 9, Application US/11238936
; Publication No. US20060025343A1
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha J.
; APPLICANT: Kavanaugh, Michael W.
; TITLE OF INVENTION: Angiogenically Effective Unit Dose of FGF and Method of
; FILE REFERENCE: 1296/12169US05
; CURRENT APPLICATION NUMBER: US/11/238,936
; CURRENT FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: US/09/417,721
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/104,103
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: Human FGF-5
US-11-238-936-9
Query Match 67.9%; Score 182; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 1,4e-164; Indels 0; Gaps 0;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 RTGSLYCRVIGGFHQLIYDGVKNGSHEANMLSVLEIFAVSQGIVGIRGVFSNKTFLAMSK 146
| | | | |
Db 85 RTGSLYCRVIGGFHQLIYDGVKNGSHEANMLSVLEIFAVSQGIVGIRGVFSNKTFLAMSK 144
QY 147 KKKLHASAKFTDDCKRRRPOENSNTYASAIHRTKTKGREMYVALNKRGAKKGCSPRV 206
| | | | |
Db 145 KKKLHASAKFTDDCKRRRPOENSNTYASAIHRTKTKGREMYVALNKRGAKKGCSPRV 204
QY 207 KQOIHSTHLPKFKOSEQBELSFTVTVPEKKKPPSPDKPILPSAPRKNTNSVYKRLKFR 266
| | | | |
Db 205 KQOIHSTHLPKFKOSEQBELSFTVTVPEKKKPPSPDKPILPSAPRKNTNSVYKRLKFR 264
QY 267 FG 268
| |
Db 265 FG 266
RESULT 6
US-11-134-703-8
; Sequence 8, Application US/11134703
; Publication No. US20060009393A1
; GENERAL INFORMATION:
; APPLICANT: Hanada et al.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT APPLICATION NUMBER: US/11/134,703
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427,920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089,485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 8
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-703-8
Query Match 65.7%; Score 176; DB 7; Length 176;
Best Local Similarity 100.0%; Pred. No. 4,6e-159;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 CRVIGGFHQLIYDGVKNGSHEANMLSVLEIFAVSQGIVGIRGVFSNKTFLAMSKKKGLHA 152
| | | | |
Db 1 CRVIGGFHQLIYDGVKNGSHEANMLSVLEIFAVSQGIVGIRGVFSNKTFLAMSKKKGLHA 60
QY 153 SAKFTDDCKRRRPOENSNTYASAIHRTKTKGREMYVALNKRGAKKGCSPRVKKPQHIS 212
| | | | |
Db 61 SAKFTDDCKRRRPOENSNTYASAIHRTKTKGREMYVALNKRGAKKGCSPRVKKPQHIS 120
QY 213 THFLPRFKQSEQBELSFTVTVPEKKKPPSPDKPILPSAPRKNTNSVYKRLKFRFG 268
| | | | |
Db 121 THFLPRFKQSEQBELSFTVTVPEKKKPPSPDKPILPSAPRKNTNSVYKRLKFRFG 176
RESULT 7
US-11-238-936-15
; Sequence 15, Application US/11238936
; Publication No. US20060025343A1
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha J.
; APPLICANT: Kavanaugh, Michael W.
; TITLE OF INVENTION: Angiogenically Effective Unit Dose of FGF and Method of
; FILE REFERENCE: 1296/12169US05
; CURRENT APPLICATION NUMBER: US/11/238,936
; CURRENT FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: US/09/417,721
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/104,103
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human FGF-5
US-11-238-936-15
Query Match 56.3%; Score 151; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 3e-135;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 RTGSLYCRVIGGFHQLIYDGVKNGSHEANMLSVLEIFAVSQGIVGIRGVFSNKTFLAMSK 146
| | | | |
Db 85 RTGSLYCRVIGGFHQLIYDGVKNGSHEANMLSVLEIFAVSQGIVGIRGVFSNKTFLAMSK 144
QY 147 KKKLHASAKFTDDCKRRRPOENSNTYASAIHRTKTKGREMYVALNKRGAKKGCSPRV 206
| | | | |
Db 145 KKKLHASAKFTDDCKRRRPOENSNTYASAIHRTKTKGREMYVALNKRGAKKGCSPRV 204
QY 207 KQOIHSTHLPKFKOSEQBELSFTVTVPEKK 237
| | | | |
Db 205 KQOIHSTHLPKFKOSEQBELSFTVTVPEKK 235
RESULT 8
US-11-134-703-6
; Sequence 6, Application US/11134703
; Publication No. US20060009393A1
; GENERAL INFORMATION:

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/ APPLICANT: Hanada et al.
/ TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
/ FILE REFERENCE: 67015-05
/ CURRENT APPLICATION NUMBER: US/11/134,703
/ PRIOR FILING DATE: 2005-05-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/37065
/ PRIOR FILING DATE: 2003-11-19
/ PRIOR APPLICATION NUMBER: US 60/427,920
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: US 10/089,485
/ PRIOR FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26689
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/157,103
/ PRIOR FILING DATE: 1999-10-02
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 6
/ LENGTH: 176
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-134-703-6

Query Match          54.1%; Score 145; DB 7; Length 176;
Best Local Similarity 100.0%; Pred. No. 9,9e-130;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CRVGGFHHQIYIPDGKVNKSGNSHEANMLSVLEIFPVSGSIGIYIGVPSNKKFLAMSKKKGLA 152
   |||
DB 1 CRVGGFHHQIYIPDGKVNKSGNSHEANMLSVLEIFPVSGSIGIYIGVPSNKKFLAMSKKKGLA 60
   |||

QY 153 SAKFTDCKFRERFOENSNTYASAIHRTKTEGREWYVALNKGKAKGCSPRVKQHHIS 212
   |||
DB 61 SAKFTDCKFRERFOENSNTYASAIHRTKTEGREWYVALNKGKAKGCSPRVKQHHIS 120
   |||

QY 213 THFLPRFKOSEQPELSFTYTVPEKK 237
   |||
DB 121 THFLPRFKOSEQPELSFTYTVPEKK 145
   |||

RESULT 9
US-11-134-703-19
/ Sequence 19, Application US/11/134,703
/ Publication No. US20060009393A1
/ GENERAL INFORMATION:
/ APPLICANT: Hanada et al.
/ TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
/ FILE REFERENCE: 67015-05
/ CURRENT APPLICATION NUMBER: US/11/134,703
/ CURRENT FILING DATE: 2005-05-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/37065
/ PRIOR FILING DATE: 2003-11-19
/ PRIOR APPLICATION NUMBER: US 60/427,920
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: US 10/089,485
/ PRIOR FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26689
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/157,103
/ PRIOR FILING DATE: 1999-10-02
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 19
/ LENGTH: 60
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-134-703-19

Query Match          22.4%; Score 60; DB 7; Length 60;
Best Local Similarity 100.0%; Pred. No. 9.8e-50;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 KFRERFOENSNTYASAIHRTKTEGREWYVALNKGKAKGCSPRVKQHHIS 220
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DB 1 KFRERFOENSNTYASAIHRTKTEGREWYVALNKGKAKGCSPRVKQHHIS 60
   |||
RESULT 10
US-11-134-703-37
/ Sequence 37, Application US/11/134,703
/ Publication No. US20060009393A1
/ GENERAL INFORMATION:
/ APPLICANT: Hanada et al.
/ TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
/ FILE REFERENCE: 67015-05
/ CURRENT APPLICATION NUMBER: US/11/134,703
/ CURRENT FILING DATE: 2005-05-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/37065
/ PRIOR FILING DATE: 2003-11-19
/ PRIOR APPLICATION NUMBER: US 60/427,920
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: US 10/089,485
/ PRIOR FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26689
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/157,103
/ PRIOR FILING DATE: 1999-10-02
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 37
/ LENGTH: 52
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Variant peptide sequence.
US-11-134-703-37

Query Match          19.4%; Score 52; DB 7; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.2e-42;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 KFRERFOENSNTYASAIHRTKTEGREWYVALNKGKAKGCSPRVKQHHIS 212
   |||
DB 1 KFRERFOENSNTYASAIHRTKTEGREWYVALNKGKAKGCSPRVKQHHIS 52
   |||

RESULT 11
US-11-134-703-38
/ Sequence 38, Application US/11/134,703
/ Publication No. US20060009393A1
/ GENERAL INFORMATION:
/ APPLICANT: Hanada et al.
/ TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
/ FILE REFERENCE: 67015-05
/ CURRENT APPLICATION NUMBER: US/11/134,703
/ CURRENT FILING DATE: 2005-05-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/37065
/ PRIOR FILING DATE: 2003-11-19
/ PRIOR APPLICATION NUMBER: US 60/427,920
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: US 10/089,485
/ PRIOR FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26689
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/157,103
/ PRIOR FILING DATE: 1999-10-02
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 38
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Variant peptide sequence.
US-11-134-703-38
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Query Match 18.3%; Score 49; DB 7; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.1e-39; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 NTYASAIHRTKTKGREWYVALNKRKAGCSPRVKPOHISTHFLPRFK 220
Db 1 NTYASAIHRTKTKGREWYVALNKRKAGCSPRVKPOHISTHFLPRFK 49

RESULT 12

US-11-134-703-36
; Sequence 36, Application US/11134703
; Publication No. US20060009393A1
; GENERAL INFORMATION:

; APPLICANT: Hanada et al.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT APPLICATION NUMBER: US/11/134,703
; PRIOR FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427,920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089,485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 36
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant peptide sequence.
US-11-134-703-36

Query Match 17.9%; Score 48; DB 7; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8e-38; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 TYASAIHRTKTKGREWYVALNKRKAGCSPRVKPOHISTHFLPRFK 220
Db 1 TYASAIHRTKTKGREWYVALNKRKAGCSPRVKPOHISTHFLPRFK 48

RESULT 13

US-11-134-703-32
; Sequence 32, Application US/11134703
; Publication No. US20060009393A1
; GENERAL INFORMATION:

; APPLICANT: Hanada et al.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES FOR FIBROBLAST GROWTH FACTOR 5 (FGF-5)
; FILE REFERENCE: 67015-05
; CURRENT APPLICATION NUMBER: US/11/134,703
; PRIOR FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: PCT/US2003/37065
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/427,920
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 10/089,485
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26689
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,103
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 32
; LENGTH: 10
; TYPE: PRT

; ORGANISM: homo sapiens
US-11-134-703-32

Query Match 3.7%; Score 10; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0039; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 MTSVLEIFAV 126
Db 1 MTSVLEIFAV 10

RESULT 14

US-11-087-099-8568
; Sequence 8568, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B RP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8568
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Sorghum bicolor
US-11-087-099-8568

Query Match 3.4%; Score 9; DB 7; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 SASSSPAS 66
Db 114 SASSSPAS 122

RESULT 15

US-11-096-568A-20771
; Sequence 20771, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20771
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc_feature
; LOCATION: (1)..(413)
; OTHER INFORMATION: Ceres Seq. ID no. 12387083
US-11-096-568A-20771

Query Match 3.4%; Score 9; DB 7; Length 413;
Best Local Similarity 100.0%; Pred. No. 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 SSSASASP 63
Db 243 SSSASASP 251

Search completed: April 11, 2006, 03:46:10
Job time : 10.5 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 03:36:56 ; Search time 13 seconds
(without alignments)
1985.546 Million cell updates/sec

Title: US-10-089-485-18

Perfect score: 268

Sequence: 1 MSLSFLLLFPSHLLLSAWA.....LSAPKNTNSVYKRLKPRG 268

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	56.3	267	1 TVHUF5	fibroblast growth
2	90	33.6	264	2 A36207	fibroblast growth
3	90	33.6	266	2 S68144	fibroblast growth
4	39	14.6	121	2 S68145	fibroblast growth
5	10	3.7	109	2 S69307	probable membrane
6	9	3.4	143	2 T22906	hypothetical prote
7	9	3.4	979	2 T01566	hypothetical prote
8	3	3.0	153	2 S67294	hypothetical prote
9	8	3.0	202	1 TVMHS	fibroblast growth
10	8	3.0	206	1 TVHUS	fibroblast growth
11	8	3.0	206	2 S24268	fibroblast growth
12	8	3.0	208	2 S20102	fibroblast growth
13	8	3.0	208	2 S14192	fibroblast growth
14	8	3.0	225	2 B84653	TIN1-like AP2 doma
15	8	3.0	229	2 JC7219	nuclear protein SR
16	8	3.0	238	2 S77699	inner cell wall ma
17	8	3.0	238	2 D84585	hypothetical prote
18	8	3.0	262	2 T40941	hypothetical serin
19	8	3.0	264	2 D96694	hypothetical prote
20	8	3.0	268	2 C84585	hypothetical prote
21	8	3.0	270	2 F86170	GBF4 [imported] -
22	8	3.0	299	2 TS2452	ATP-dependent Clp
23	8	3.0	325	2 H96815	hypothetical prote
24	8	3.0	354	2 S39406	homeotic protein
25	8	3.0	391	2 S61704	probable transcrip
26	8	3.0	396	2 T26987	hypothetical prote
27	8	3.0	412	2 S30299	Krox-20 protein -
28	8	3.0	419	2 T49292	hypothetical prote
29	8	3.0	429	2 A47305	translation initia

30	8	3.0	431	2 T12450	hypothetical prote
31	8	3.0	459	2 A88712	protein C17H12.9 (
32	8	3.0	472	2 T04699	hypothetical prote
33	8	3.0	484	2 S66713	hypothetical prote
34	8	3.0	490	2 A32140	steroid 15beta-mon
35	8	3.0	559	1 RMBYS1	glycophospholipid-
36	8	3.0	600	2 S07638	spore coat protein
37	8	3.0	640	1 COBEU2	UL35 protein - hum
38	8	3.0	640	2 S62747	homeotic protein A
39	8	3.0	661	2 T16597	hypothetical prote
40	8	3.0	717	2 T25431	hypothetical prote
41	8	3.0	741	2 I48694	probable transcrip
42	8	3.0	742	2 A49672	transcription fact
43	8	3.0	772	2 A55004	transcription fact
44	8	3.0	775	1 EDBE11	transcription fact
45	8	3.0	825	1 EDBEXD	immediate-early pr

ALIGNMENTS

RESULT 1
TVHUF5
fibroblast growth factor 5 - human
N:Alternate names: transforming protein FGFS
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A31194
R:Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Mol. Cell. Biol. 8, 3487-3495, 1988
A:Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth t
A:Reference number: A31194; MUID:89096942; PMID:3211147
A:Accession: A31194
A:Molecule type: mRNA
A:Residues: 1-267 <ZHA>
A:Cross-references: UNIPROT:P12034; UNIPARC:UPI00000462BB; GB:M23536; GB:M21617; NID:gtf
C:Genes:
A:Gene: GDB:RGFS
A:Cross-references: GDB:119907; OMIM:165190
A:Map position: 4q21-4q21
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e-139; Indels 0; Gaps 0;
Matches 151; Conservative 0; Mismatches 0;

QY 87 RTGSLYCRVIGIFHQLIYDPDGKVNQSHANMLSVLEIFAVSQGIVGIRGVFNKFLAMSK 146
|||||
DB 86 RTGSLYCRVIGIFHQLIYDPDGKVNQSHANMLSVLEIFAVSQGIVGIRGVFNKFLAMSK 145

QY 147 KCKLHASAKFTDDCKFRFRPOENSNTYASAIHRTKTKGREWYVALNKRKAKRGCSPRV 206
146 KCKLHASAKFTDDCKFRFRPOENSNTYASAIHRTKTKGREWYVALNKRKAKRGCSPRV 205

QY 207 KPOHISTHPLPRFKSQSEPELSFTTVPEBK 237
|||||
DB 206 KPOHISTHPLPRFKSQSEPELSFTTVPEBK 236

RESULT 2
A36207
fibroblast growth factor 5 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: A36207; B37360
R:Hard, O.; Drucker, B.; Goldfarb, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 8022-8026, 1990
A:Title: Expression of the murine fibroblast growth factor 5 gene in the adult central r
A:Reference number: A36207; MUID:91045929; PMID:1700424
A:Accession: A36207
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA

```

A:Residues: 1-264 <HAU>
A:Cross-references: UNIPROT:P15656; UNIPARC:UPI0000003F7B; GB:M37821; GB:M37822; GB:M378
R:Hebert, J.M.; Baillico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A:Reference number: A37360; MUID:90201563; PMID:2318343
A:Accession: B37360
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <HEB>
A:Cross-references: UNIPARC:UPI0000003F7B; GB:M30643; NID:g193294; PIDN:AAA36698.1; PID:
C:Superfamily: fibroblast growth factor

Query Match          33.6%; Score 90; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 1.3e-79;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LEIFAVSQIGIRGVFSNKKFLAMSKKGLHASAKETDDCKFRERQENSNTYASAIHR 180
    |||||
DB 119 LEIFAVSQIGIRGVFSNKKFLAMSKKGLHASAKETDDCKFRERQENSNTYASAIHR 178
    |||||

QY 181 TEXTGREWYVALNKGKAKRGCSPRVKPOH 210
    |||||
DB 179 TEXTGREWYVALNKGKAKRGCSPRVKPOH 208
    |||||

RESULT 3
S68144
fibroblast growth factor 5 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68144
R:Harfor, Y.; Yamaoka, M.; Itoh, N.
Biochim. Biophys. Acta 1306, 31-33, 1996
A:Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel tr
A:Reference number: S68144; MUID:96201703; PMID:8611621
A:Accession: S68144
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-266 <HAT>
A:Cross-references: UNIPROT:P48807; UNIPARC:UPI000012A716; EMBL:D64085; NID:g992952; PID
C:Superfamily: fibroblast growth factor

Query Match          33.6%; Score 90; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.3e-79;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LEIFAVSQIGIRGVFSNKKFLAMSKKGLHASAKETDDCKFRERQENSNTYASAIHR 180
    |||||
DB 119 LEIFAVSQIGIRGVFSNKKFLAMSKKGLHASAKETDDCKFRERQENSNTYASAIHR 178
    |||||

QY 181 TEXTGREWYVALNKGKAKRGCSPRVKPOH 210
    |||||
DB 179 TEXTGREWYVALNKGKAKRGCSPRVKPOH 208
    |||||

RESULT 4
S68145
fibroblast growth factor 5, truncated splice form - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68145
R:Harfor, Y.; Yamaoka, M.; Itoh, N.
Biochim. Biophys. Acta 1306, 31-33, 1996
A:Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel tr
A:Reference number: S68144; MUID:96201703; PMID:8611621
A:Accession: S68145
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-121 <HAT>
A:Cross-references: UNIPROT:P48807; UNIPARC:UPI000002A98F; EMBL:D64086; NID:g987689; PID
C:Keywords: alternative splicing

```

```

Query Match          14.6%; Score 39; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 3e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 SSFQWSPSGRRTGSLYCVGIGFHLQIYDPDGKNGSHEA 115
    |||||
DB 75 SSFQWSPSGRRTGSLYCVGIGFHLQIYDPDGKNGSHEA 113
    |||||

RESULT 5
S69307
probable membrane protein YLR294c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein I6003.19-a
C:Species: Saccharomyces cerevisiae
C>Date: 20-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: S69307
R:Pauley, A.
submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid 8003.
A:Reference number: S50366
A:Accession: S69307
A:Molecule type: DNA
A:Residues: 1-109 <PAU>
A:Cross-references: UNIPROT:O13543; UNIPARC:UPI000004F949; EMBL:U17243; NID:g596030; PID
C:Genetics:
A:Gene: MIPS:YLR294c
A:Cross-references: SGD:S0004285
A:Map position: 12R
C:Superfamily: Saccharomyces probable membrane protein YLR294c
C:Keywords: transmembrane protein
F:77-93/Domain: transmembrane #status predicted <TM>

Query Match          3.7%; Score 10; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLSFLLLP 11
    |||||
DB 82 SLSFLLLP 91
    |||||

RESULT 6
T22906
hypothetical protein F58D12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22906
R:Percy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19635
A:Accession: T22906
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-143 <WIL>
A:Cross-references: UNIPROT:O02276; UNIPARC:UPI00000753E8; EMBL:Z81092; PIDN:CAB03144.1;
A:Experimental source: clone F58D12
C:Genetics:
A:Gene: CESP:F58D12.1
A:Map position: 5
A:Introns: 14/1; 38/2; 75/1; 90/3

Query Match          3.4%; Score 9; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SSSASSSPA 64
    |||||
DB 53 SSSASSSPA 61
    |||||

RESULT 7
T01566
hypothetical protein A_TW018A10.23 - Arabidopsis thaliana

```

C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01566
R:Dempey, S.; Harper, M.
Submitted to the EMBL Data Library, July 1997
A:Description: The sequence of A. thaliana TM018A10.
A:Reference number: Z14348
A:Accession: T01566
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-979 <DEM>
A:Cross-references: UNIPROT:Q23096; UNIPARC:UPI000009B61; EMBL:AF013294; NID:G2252848;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 466/3; 569/3; 649/3; 688/1; 740/3; 877/3
A>Note: A_TM018A10.23
C:Superfamily: Arabidopsis thaliana hypothetical protein A_TM018A10.23

Query Match 3.4%; Score 9; DB 2; Length 979;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 SSSASASP 63
|||||
Db 37 SSSASASP 45

RESULT 8
S67294
hypothetical protein YOR382w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O6760
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C:Accession: S67294
R:Deilus, H.; Hebling, U.; Hofmann, B.
Submitted to the Protein Sequence Database, July 1996
A:Reference number: S67261
A:Accession: S67294
A:Molecule type: DNA
A:Residues: 1-153
A:Cross-references: UNIPROT:Q08906; UNIPARC:UPI000004F973; EMBL:Z75290; NID:G1420822; PI
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:FIT2; MIPS:YOR382w
A:Cross-references: SGD:S0005909
A:Map position: 15R

Query Match 3.0%; Score 8; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 SSSASASP 62
|||||
Db 122 SSSASASP 129

RESULT 9
TMSHS
fibroblast growth factor 4 - mouse
N:Alternate names: transforming protein hsf1; transforming protein k-RGF; transforming
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: S04741; A37360
R:Brookes, S.; Smith, R.; Thurlow, J.; Dickson, C.; Peters, G.
Nucleic Acids Res. 17, 4037-4045, 1989
A:Title: The mouse homologue of hsf/k-RGF: sequence, genome organization and location re
A:Reference number: S04741; MUID:89296455; PMID:2740210
A:Accession: S04741
A:Molecule type: DNA
A:Residues: 1-202 <BRO>
A:Cross-references: UNIPROT:P11403; UNIPARC:UPI0000027966; GB:X14849; GB:M28516; NID:G52
R:Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.

Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse RGF family members and characterization
A:Reference number: A37360; MUID:90201563; PMID:2318343
A:Accession: A37360
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166 'S', 168-202 <HEB>
A:Cross-references: UNIPARC:UPI000000415D; GB:M30642; NID:G193290; PIDN:AAA7619.1; PID:
C:Genetics:
A:Gene: hsf
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match 3.0%; Score 8; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 VGIGFHQ 102
|||||
Db 86 VGIGFHQ 93

RESULT 10
TVHUS
fibroblast growth factor 4 - human
N:Alternate names: heparin secretory transforming protein 1; Kaposi sarcoma oncogene; tr
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A28417; A29876; A29649
R:Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Sugl
Proc. Natl. Acad. Sci. U.S.A. 84, 7305-7309, 1987
A:Title: Genomic sequence of hsf, a transforming gene encoding a protein homologous to E
A:Reference number: A28417; MUID:88041096; PMID:2959959
A:Accession: A28417
A:Molecule type: DNA
A:Residues: 1-206 <YOS>
A:Cross-references: UNIPROT:P08620; UNIPARC:UPI0000040662; DBJ:J02986; NID:G184430; PI
R:Taira, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A:Title: cDNA sequence of human transforming gene hsf and identification of the coding se
A:Reference number: A29876; MUID:87204251; PMID:2953031
A:Accession: A29876
A:Molecule type: mRNA
A:Residues: 1-206 <TAI>
A:Cross-references: UNIPARC:UPI0000040662; GB:J02986; GB:M16338; NID:G184430; PIDN:AA59
R:Deilli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.
Cell 50, 729-737, 1987
A:Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth f
A:Reference number: A29649; MUID:87301716; PMID:2957062
A:Accession: A29649
A:Molecule type: mRNA
A:Residues: 1-206 <BOV>
A:Cross-references: UNIPARC:UPI0000040662; GB:M17446; NID:G186785; PIDN:AAA59473.1; PID:
A:Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the mou
C:Genetics:
A:Gene: GDB:FGF4; HSTF1
A:Cross-references: GDB:120066; OMIM:164980
A:Map position: 11q13.3-11q13.3
A:Introns: 114/1; 148/3
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; Kaposi sarcoma; transforming protein

Query Match 3.0%; Score 8; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 VGIGFHQ 102
|||||
Db 90 VGIGFHQ 97

RESULT 11
JC4268

fibroblast growth factor 4 - bovine
N:Alternate names: transforming protein hsc
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
R:Yu, J.C.; Desabara, A.U.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Miki, T.; Heidaran, Gene 162, 333-334, 1995
A>Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hsc.
A:Reference number: JG4268; MUID:96032369; PMID:7557455
A:Accession: JG4268
A:Molecule type: mRNA
A:Residues: 1-206 <YU>
A:Cross-references: UNIPARC:UPI0000176539; GB:U15969
A>Note: The authors translated the codon GGC for residue 114 as Ser
C:Comment: This protein is a member of fibroblast growth factor family. The hscgene in C
C:Genetics:
A:Gene: hsc
A:Introns: 113/3; 145/2
C:Superfamily: fibroblast growth factor
C:Keywords: thymus; transforming protein

Query Match 3.0%; Score 8; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 VGIGFHLQ 102
DB 90 VGIGFHLQ 97

RESULT 12
S20102
fibroblast growth factor 6 precursor - human
N:Alternate names: fibroblast growth factor-related protein FGF.6; transforming protein
C:Species: Homo sapiens (man)
C>Date: 18-Feb-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
A:Accession: S20102; S23739; S04204; S36910
R:Coulter, F.; Baloz, M.; Matice, I.; de Lapeyriere, O.; Blumberg, D.
Oncogene 6, 1437-1444, 1991
A>Title: Putative structure of the FGF6 gene product and role of the signal peptide.
A:Reference number: S20102; MUID:91360279; PMID:1886714
A:Accession: S20102
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-208 <COU>
A:Cross-references: UNIPROT:P10767; UNIPARC:UPI0000411BF; EMBL:X57075
A>Note: It is uncertain whether Met-1, Met-11 or Met-34 is the initiator
R:Ida, S.; Yoshida, T.; Naito, K.; Sakamoto, H.; Katoh, O.; Hirohashi, S.; Sato, T.; On Oncogene 7, 303-309, 1992
A>Title: Human hsc-2 (FGF-6) oncogene: cDNA cloning and characterization.
A:Reference number: S23739; MUID:92195660; PMID:1549352
A:Accession: S23739
A:Molecule type: mRNA
A:Residues: 1-208 <ID>
A:Cross-references: UNIPARC:UPI0000411BF; EMBL:X63454
A>Note: It is uncertain whether Met-1 or Met-11 is the initiator
R:Matice, I.; Adelaide, J.; Raynaud, F.; Mattei, M.G.; Coulter, F.; Planche, J.; de Lape Oncogene 4, 335-340, 1989
A>Title: Characterization of the HST-related FGF.6 gene, a new member of the fibroblast A:Reference number: S04204; MUID:89201880; PMID:2649847
A:Accession: S04204
A:Molecule type: DNA
A:Residues: 81-99, 'G', 101-208 <MAR>
A:Cross-references: UNIPARC:UPI000016A8P6; EMBL:X14071; NID:G31354; PIDN:CA837648.2; PID C:Genetics:
A:Gene: GDB:FGF6; hsc-2
A:Cross-references: GDB:119908; OMIM:134921
A:Map position: 12p13-12p13
A:Introns: 115/3; 150/2
C:Superfamily: fibroblast growth factor
F:1-40/Domain: (or 11-40 or 34-40) signal sequence #status predicted <SIG>
F:41-208/Product: fibroblast growth factor 6 #status predicted <MAT>

Query Match 3.0%; Score 8; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 VGIGFHLQ 102
DB 92 VGIGFHLQ 99

RESULT 13
S14192
fibroblast growth factor 6 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
A:Accession: S14192; I49665; I49664
R:de Lapeyriere, O.; Rosnet, O.; Benharroch, D.; Raynaud, F.; Marchetto, S.; Planche, J. Oncogene 5, 823-831, 1990
A>Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.
A:Reference number: S14192; MUID:90295275; PMID:2193291
A:Accession: S14192
A:Molecule type: DNA
A:Residues: 1-208 <LAB>
A:Cross-references: UNIPROT:P21658; UNIPARC:UPI000020A67; EMBL:X51552
A>Note: It is uncertain whether Met-1 or Met-11 is the initiator
R:Ollendorff, V.; Rosnet, O.; Matice, I.; Blumberg, D.; deLapeyriere, O. Biochimie 74, 1035-1038, 1992
A>Title: Isolation and sequence of the murine Fgf6 cDNA.
A:Reference number: I49664; MUID:93120244; PMID:1477139
A:Accession: I49665
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 19-208 <RES>
A:Cross-references: UNIPARC:UPI00016CD51; GB:M92416; NID:G193288; PIDN:AAA62261.1; PID: A:Accession: I49664
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: UNIPARC:UPI00016CD50; GB:M92415; NID:G193286; PIDN:AAA62260.1; PID: C:Genetics:
A:Gene: Fgf6
A:Introns: 116/1; 150/3
A:Superfamily: fibroblast growth factor

Query Match 3.0%; Score 8; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 VGIGFHLQ 102
DB 92 VGIGFHLQ 99

RESULT 14
B84653
TINY-like AP2 domain transcription factor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
A:Accession: B84653
R:Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Xoo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon, L. eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: B84420; MUID:20083487; PMID:10617197
A:Accession: B84653
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225 <STO>
A:Cross-references: UNIPROT:O82315; UNIPARC:UPI0000179899; GB:AE002093; NID:G3643601; PI C:Genetics:
A:Gene: At2g25820
A:Map position: 2

Query Match 3.0%; Score 8; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 55 SSSSSASS 62
 |||||
 Db 140 SSSSSASS 147

RESULT 15

JC7219
 nuclear protein SR-25 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C/Accession: JC7219
 R:Sasahara, K.; Yamaoka, T.; Moritani, M.; Tanaka, M.; Iwahana, H.; Yoshimoto, K.; Miyag
 Biochem. Biophys. Res. Commun. 269, 444-450, 2000
 A/Title: Molecular cloning and expression analysis of a putative nuclear protein, SR-25.
 A/Reference number: JC7219; MUID:20175222; PMID:10708573
 A/Accession: JC7219
 A/Molecule type: mRNA
 A/Residues: 1-229 <SAS>
 A/Cross-references: UNIPROT:Q9JW93; UNIPARC:UPI00000231C4; DDBJ:AB035383; NID:g7619895;
 A/Experimental source: MIN6 cell line
 C/Comment: This protein is a highly hydrophilic nuclear protein with a serine-arginine r
 A splicing factors.
 C/Keywords: nucleus; RNA processing

Query Match 3.0%; Score 8; DB 2; Length 229;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 55 SSSSSASS 62
 |||||
 Db 77 SSSSSASS 84

Search completed: April 11, 2006, 03:38:26
 Job time : 13 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 03:33:26 ; Search time 73 Seconds
(without alignments) 2590.159 Million cell updates/sec

Title: US-10-089-485-18

Perfect score: 268
Sequence: 1 MSISFLILFFSHLILSAMA.....LSAPRKNTNSVKYKRLKRFEG 268

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	100.0	268	2 Q8NF90 HUMAN	Q8NF90 homo sapien
2	237	88.4	268	1 FGFS_HUMAN	P12034 homo sapien
3	125	46.6	125	2 Q8NBG6 HUMAN	Q8NBG6 homo sapien
4	119	44.4	129	2 Q6A549 HUMAN	Q6A549 homo sapien
5	90	33.6	264	1 FGFS_MOUSE	P15656 mus musculu
6	90	33.6	266	1 FGFS_RAT	P48807 rattus norv
7	60	22.4	153	2 Q8S073 CANFA	Q8S073 canis faml
8	30	11.2	99	2 Q6XK01 RABIT	Q6XK01 oryctolagus
9	29	10.8	79	2 Q6XK00 RABIT	Q6XK00 oryctolagus
10	21	7.8	225	2 Q5TLE2 BRARE	Q5TLE2 brachydanto
11	19	7.1	230	2 Q4RPO6 TERNING	Q4RPO6 tetradodon n
12	16	6.0	87	2 Q8BN07 CANFA	Q8BN07 canis faml
13	13	3.7	109	2 Q13543 YEAST	Q13543 saccharomyc
14	10	3.7	349	2 Q7Y0C1 ORYSA	Q7Y0C1 oryza sativ
15	10	3.7	418	2 Q54TY7 DICDI	Q54TY7 dictyostell
16	10	3.7	420	2 Q76853 DROME	Q76853 dictyostell
17	10	3.7	420	2 Q9V356 DROME	Q9V356 dictyostell
18	10	3.7	706	2 Q8S2H3 DROME	Q8S2H3 drosophila
19	10	3.7	706	2 Q8EBR3 DROME	Q8EBR3 drosophila
20	9	3.4	140	2 Q8S1P2 ORYSA	Q8S1P2 oryza sativ
21	9	3.4	143	2 Q02276 CAEBL	Q02276 caenorhabdi
22	9	3.4	168	2 Q9J173 MOUSE	Q9J173 mus musculu
23	9	3.4	180	2 Q4T440 TERNING	Q4T440 tetradodon n
24	9	3.4	181	2 Q4TEY6 TERNING	Q4TEY6 tetradodon n
25	9	3.4	188	2 Q8S444 SOEBI	Q8S444 sorghum bic
26	9	3.4	209	2 Q5WFO8 DICLA	Q5WFO8 dicentrarch
27	9	3.4	233	2 Q6DCP9 XENLA	Q6DCP9 xenopus lae
28	9	3.4	284	2 Q71SY8 CHICK	Q71SY8 gallus gall
29	9	3.4	295	1 U9166_HUMAN	U9166 homo sapien
30	9	3.4	295	1 U9166_MOUSE	U9166 mus musculu
31	9	3.4	295	2 Q5W0G8_HUMAN	Q5W0G8 homo sapien

32	9	3.4	482	2 Q7S0U9 NEURC	Q7S0U9 neurospora
33	9	3.4	492	2 Q4QB77 LEIMA	Q4QB77 leishmania
34	9	3.4	492	2 Q8BS05 MOUSE	Q8BS05 mus musculu
35	9	3.4	495	2 Q5VZ18 HUMAN	Q5VZ18 homo sapien
36	9	3.4	526	2 Q9ZRH9 ORYSA	Q9ZRH9 oryza sativ
37	9	3.4	540	2 Q6S0Z7 ORYSA	Q6S0Z7 oryza sativ
38	9	3.4	553	2 Q7TML6 MOUSE	Q7TML6 mus musculu
39	9	3.4	565	2 Q6Z9D7 ORYSA	Q6Z9D7 oryza sativ
40	9	3.4	648	2 Q6ZER3 ORYSA	Q6ZER3 oryza sativ
41	9	3.4	712	2 Q6FWG1 CANGA	Q6FWG1 candida gla
42	9	3.4	719	2 Q6DJ90 XENTR	Q6DJ90 xenopus tro
43	9	3.4	745	2 Q86NY8 DROME	Q86NY8 drosophila
44	9	3.4	749	2 Q8DAV3 VIBVU	Q8DAV3 vibrio vuln
45	9	3.4	749	2 Q7MJ05_VIBBY	Q7MJ05 vibrio vuln

ALIGNMENTS

RESULT 1
Q8NF90 HUMAN
ID Q8NF90 HUMAN PRELIMINARY; PRT; 268 AA.
AC Q8NF90;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Fibroblast growth factor 5, isoform 1.
GN Name=FGF5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OK NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21347229; PubMed=11454700;
RA Hanada K.-I., Perry-Lalley D.M., Ohnmacht G.A., Bettinotti M.P., Yang J.C.;
RT "Identification of fibroblast growth factor-5 as an overexpressed antigen in multiple human adenocarcinomas";
RL Cancer Res. 61:5511-5516(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Hanada K.-I., Yang J.C.;
RN Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Reinhold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Ditchenko L., Murnighan K., Farmer A.A., Rubin A.G., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R., Brownstein M.J., Ueda T.B., Toshimiyuki S., Carrino P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Boeak S.A., McEwen P.J., McKernan K.J., Malek J.A., Guarnarathne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B., Scherch A., Schein J.B., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=lung;
RC Director MGC Project;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF531149; AAN04097.1; -; mRNA.
 DR EMBL; BC074858; AAN74858.1; -; mRNA.
 DR EMBL; BC074859; AAN74859.1; -; mRNA.
 DR HSP; P08620; I107.
 DR GO; GO:0008083; F;growth factor activity; IEA.
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00263; HBGF.FGF.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD00831; IL1_HBGF; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
 KW Growth factor.
 SQ SEQUENCE 268 AA; 29551 MW; 2887268B26781BCF CRC64;
 Query Match 100.0%; Score 268; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 5e-253;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLSFLLLFFSHLLISAAHGEKRLAPKGPAPATDNNPRGSSSSSSAMSSSSAS 60
 DB 1 MSLSFLLLFFSHLLISAAHGEKRLAPKGPAPATDNNPRGSSSSSSAMSSSSAS 60
 QY 61 SSPAASLSGSGSGLSESSFPQWSPSGRRTSLYCRVIGIFHLQIYPPGKYNHSEANMLSV 120
 DB 61 SSPAASLSGSGSGLSESSFPQWSPSGRRTSLYCRVIGIFHLQIYPPGKYNHSEANMLSV 120
 QY 121 LEIFAVSQGIVGIRGVFNKFLAMSCKGLHASAKETDDCKTREPQENSNTYTAIAHR 180
 DB 121 LEIFAVSQGIVGIRGVFNKFLAMSCKGLHASAKETDDCKTREPQENSNTYTAIAHR 180
 QY 121 LEIFAVSQGIVGIRGVFNKFLAMSCKGLHASAKETDDCKTREPQENSNTYTAIAHR 180
 DB 181 TEKTGRWVVALNKGKARCGSPRYKPHISTHPLPRKQSBQBLSTTVVPEKKRP 240
 QY 181 TEKTGRWVVALNKGKARCGSPRYKPHISTHPLPRKQSBQBLSTTVVPEKKRP 240
 DB 241 SPIKPIPLSAPRKNTSNVYKRLKPRFG 268
 QY 241 SPIKPIPLSAPRKNTSNVYKRLKPRFG 268
 DB 241 SPIKPIPLSAPRKNTSNVYKRLKPRFG 268
 RESULT 2
 FGF5_HUMAN STANDARD; PRT; 268 AA.
 ID FGF5_HUMAN STANDARD; PRT; 268 AA.
 AC P12034; O75846;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Fibroblast growth factor 5 precursor (FGF-5) (HBGF-5) (Smag-82).
 GN Name=FGF5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_Taxid=9606;
 RX MEDLINE=91045929; PubMed=1700424;
 RA Haub O., Drucker B., Goldfarb M.;
 RT "Expression of the murine fibroblast growth factor 5 gene in the adult
 RT central nervous system";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
 RN (2)
 RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
 RX MEDLINE=8906942; PubMed=3211147;
 RA Zhan X., Bates B., Hu X., Goldfarb M.;
 RT "The human FGF-5 oncogene encodes a novel protein related to
 RT fibroblast growth factors";
 RL Mol. Cell. Biol. 8:3487-3495(1988).
 RN (3)
 RP NUCLEOTIDE SEQUENCE (ISOFORM SHORT).

RA Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A., Yoneda A., Komi A.,
 RA Imanura T.;
 RT "An alternatively-spliced FGF-5 mRNA is abundant in brain and
 RT translates into a partial agonist/antagonist for FGF-5 neurotrophic
 RT activity";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP NUCLEOTIDE SEQUENCE (ISOFORM SHORT).
 RC TISSUE=umbilical artery;
 RX MEDLINE=20379035; PubMed=10823842; DOI=10.1074/jbc.M910099199;
 RA de Vries C.J.M., van Ackerberg T.A.B., Horrevorts A.J.G.,
 RA ten Cate J.W., Pannekoek H.;
 RT "Differential display identification of 40 genes with altered
 RT expression in activated human smooth muscle cells. Local expression in
 RT atherosclerotic lesions of smags, smooth muscle activation-specific
 RT genes";
 RL J. Biol. Chem. 275:23938-23947(2000).
 CC -1- FUNCTION: This oncogene is expressed in neonatal brain. FGF-5 can
 CC transform NIH 3T3 cells.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long; Sequence=Displayed;
 CC IsoId=P12034-1; Sequence=VSP_001518, VSP_001519;
 CC Name=Short; Synonyms=FGF-5;
 CC IsoId=P12034-2; Sequence=VSP_001518, VSP_001519;
 CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M37825; AAB05463.1; -; mRNA.
 CC EMBL; M23536; AAB60689.1; -; Genomic_DNA.
 CC EMBL; M23534; AAB60689.1; JOINED; Genomic_DNA.
 CC EMBL; M23535; AAB60689.1; JOINED; Genomic_DNA.
 CC EMBL; M23534; AAB60689.1; ALT_SEQ; Genomic_DNA.
 CC EMBL; AB016517; BAA3738.1; -; mRNA.
 CC EMBL; AF171928; AAF89742.1; -; mRNA.
 CC PIR; A31194; TVHUP5.
 CC HSP; P08620; I107.
 CC Ensembl; ENSG00000138675; Homo sapiens.
 CC HGNC; HGNC:3683; FGF5.
 CC MIM; 165190; -;
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0008283; P:cell proliferation; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0008543; P:fibroblast growth factor receptor signaling. . .; TAS.
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC InterPro; IPR002348; GF_heparin_bd.
 CC InterPro; IPR002348; IL1_HBGF.
 CC Pfam; PF00167; FGF; 1.
 CC PRINTS; PR00263; HBGF.FGF.
 CC PRODOM; PD00831; IL1_HBGF; 1.
 CC SMART; SM00442; FGF; 1.
 CC PROSITE; PS00247; HBGF_FGF; 1.
 KW Alternative splicing; Glycoprotein; Growth factor; Mitogen;
 KW Proto-oncogene; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 268 Fibroblast growth factor 5.
 FT COMBIAS 49 52 Poly-Ser.
 FT COMBIAS 55 62 Poly-Ser.
 FT CARBOHD 110 110 N-linked (GlcNAc...) (potential).
 FT VARSPLIC 120 123 VLEI -> QVHR (in isoform Short).
 FT VARSPLIC 124 268 /FTId=VSP_001518.
 FT VARSPLIC 124 268 Missing (in isoform Short).
 FT VARSPLIC 124 268 /FTId=VSP_001519.
 FT CONFLICT 42 42 R -> I (in Ref. 1).
 FT CONFLICT 83 86 PSGR -> LGA (in Ref. 2).
 FT SEQUENCE 268 AA; 29527 MW; 08F4268B26781E9D CRC64;

Query Match 88.4%; Score 237; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 9.9e-223;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLLLFPFSLHLLISAWAHGEKRLAPKQGPAPATDNRPNRSGSSRQSSSSAMSSSSAS 60
DB 1 MSLSFLLLLFPFSLHLLISAWAHGEKRLAPKQGPAPATDNRPNRSGSSRQSSSSAMSSSSAS 60
QY 61 SSPASISGSGSGLEQSSPQSPSGRRTSLYCRVIGIHLQIYDPGKNGSHENMLSV 120
DB 61 SSPASISGSGSGLEQSSPQSPSGRRTSLYCRVIGIHLQIYDPGKNGSHENMLSV 120
QY 121 LEIFAVSQGIIVGIRGVSNKFLAMSCKGKLHSAKFTDCKPRERQENSINTYASAIHR 180
DB 121 LEIFAVSQGIIVGIRGVSNKFLAMSCKGKLHSAKFTDCKPRERQENSINTYASAIHR 180
QY 181 TEKTRGEMTVALKRGAARCGSPRYKPOHISTHFLPRFKOSEPQLSTVTVPEKK 237
DB 181 TEKTRGEMTVALKRGAARCGSPRYKPOHISTHFLPRFKOSEPQLSTVTVPEKK 237

RESULT 3
Q8NB66 HUMAN PRELIMINARY; PRT; 125 AA.
AC Q8NB66; ID Q8NB66; DT 01-OCT-2002 (TREMBLrel. 22, Created);
DR 01-OCT-2002 (TREMBLrel. 22, Last sequence update);
DS 01-MAR-2004 (TREMBLrel. 26, Last annotation update);
OS Hypothetical protein FLN33238.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine N., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Yamamoto J., Iizuka T., Saito K., Kawai Y., Isono Y., Nakamura Y.,
Mamamoto K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
Yamazaki M., Nishimura K., Ishibashi T., Yamashita H., Murakawa K.,
Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T.,
Kusano J., Kanehori K., Takahashi-Puji A., Hara H., Tanase T.-O.,
Nomura Y., Togashi S., Komai F., Hara R., Takeuchi K., Arita M.,
Imose N., Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuma S.,
Yoshihara Y., Matsumura H., Ichihara T., Shihata N., Sano S.,
Morita S., Momiyama H., Satoh N., Takami S., Terasahima Y., Suzuki O.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujita T.,
Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs".
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK090557; BAC03477.1; -; mRNA.
DR HSSP; Q02195; IQOK.
DR GO; GO:0008083; P:growth factor activity; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF_1.

DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF_1.
DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
SQ SEQUENCE 125 AA; 14536 MW; EDBB5B1C95B6BCE CRC64;
Query Match 46.6%; Score 125; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 MSKKGKLHSAKFTDCKPRERQENSINTYASAIHRTEKTRGEMTVALKRGAARCGCS 203
DB 1 MSKKGKLHSAKFTDCKPRERQENSINTYASAIHRTEKTRGEMTVALKRGAARCGCS 203
QY 204 PRVKQOHISTHFLPRFKOSEPQLSTVTVPEKKPSPPIKPLSLAPRKNSTSVKRL 263
DB 61 PRVKQOHISTHFLPRFKOSEPQLSTVTVPEKKPSPPIKPLSLAPRKNSTSVKRL 120
QY 264 KRFPG 268
DB 121 KRFPG 125

RESULT 4
Q6A549 HUMAN PRELIMINARY; PRT; 129 AA.
AC Q6A549; ID Q6A549; DT 25-OCT-2004 (TREMBLrel. 28, Created);
DR 25-OCT-2004 (TREMBLrel. 28, Last sequence update);
DS 25-OCT-2004 (TREMBLrel. 28, Last annotation update);
DE Fibroblast growth factor 5 isoform b'.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine N., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Yamamoto J., Iizuka T., Saito K., Kawai Y., Isono Y., Nakamura Y.,
Mamamoto K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
Yamazaki M., Nishimura K., Ishibashi T., Yamashita H., Murakawa K.,
Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T.,
Kusano J., Kanehori K., Takahashi-Puji A., Hara H., Tanase T.-O.,
Nomura Y., Togashi S., Komai F., Hara R., Takeuchi K., Arita M.,
Imose N., Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuma S.,
Yoshihara Y., Matsumura H., Ichihara T., Shihata N., Sano S.,
Morita S., Momiyama H., Satoh N., Takami S., Terasahima Y., Suzuki O.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujita T.,
Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs".
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK090557; BAC03477.1; -; mRNA.
DR HSSP; Q02195; IQOK.
DR GO; GO:0008083; P:growth factor activity; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF_1.
DR ProDom; PD000831; IL1_HBGF; 1.
SQ SEQUENCE 129 AA; 13509 MW; 98C791EBA754EA2 CRC64;
Query Match 44.4%; Score 119; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e-107;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLLLFPFSLHLLISAWAHGEKRLAPKQGPAPATDNRPNRSGSSRQSSSSAMSSSSAS 60
DB 1 MSLSFLLLLFPFSLHLLISAWAHGEKRLAPKQGPAPATDNRPNRSGSSRQSSSSAMSSSSAS 60
QY 61 SSPASISGSGSGLEQSSPQSPSGRRTSLYCRVIGIHLQIYDPGKNGSHENMLSV 119
DB 61 SSPASISGSGSGLEQSSPQSPSGRRTSLYCRVIGIHLQIYDPGKNGSHENMLSV 119
RESULT 5
FGF5_MOUSE STANDARD; PRT; 264 AA.
AC P15656; ID P15656; DT 01-APR-1990 (Rel. 14, Created);
DR 01-APR-1990 (Rel. 14, Last sequence update);
DS 01-APR-1990 (Rel. 14, Last annotation update);
DE Fibroblast growth factor 5 precursor (FGF-5) (HBGF-5).
GN Name=FGF5; Synonyms=FGF-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;
 [1] NUCLEOTIDE SEQUENCE (ISOFORM LONG).
 RP MEDLINE=90201563; PubMed=2318343;
 RX Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
 RA "Isolation of cDNAs encoding four mouse FGF family members and
 RT characterization of their expression patterns during embryogenesis";
 RL Dev. Biol. 138:454-463 (1990).
 [2] NUCLEOTIDE SEQUENCE (ISOFORM LONG).
 RC STRAIN=C57BL/6;
 RX MEDLINE=91045929; PubMed=1700424;
 RA Haub O., Drucker B., Goldfarb M.;
 RT "Expression of the murine fibroblast growth factor 5 gene in the adult
 RL central nervous system";
 Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026 (1990).
 [3] NUCLEOTIDE SEQUENCE (ISOFORM SHORT).
 RX MEDLINE=99003286; PubMed=9786939; DOI=10.1074/jbc.273.44.29262;
 RA Ozawa K., Suzuki S., Asada M., Tomooka Y., Ii A.J., Yoneda A.,
 RA Kom A., Imanura T.;
 RT "An alternatively spliced fibroblast growth factor (FGF)-5 mRNA is
 RT abundant in brain and translates into a partial agonist/antagonist for
 RT FGF-5 neurotrophic activity";
 J. Biol. Chem. 273:29262-29271 (1998).
 [4] NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM LONG).
 RC STRAIN=C57BL/6; TISSUE=skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oseko N., Saito R., Suzuki H., Yamahata I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Baladrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schintl L.M., Kampin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brune V., Chochia C., Corbett L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimonod S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglocz D.R., Malata L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Peeble G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Seton M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Winding L.G., Wymshew-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 Nature 420:563-573 (2002).
 [5] NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM LONG).
 RC STRAIN=C57BL/6; TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaefer T.B.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

FAhey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Buttrigues A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.T., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schin J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [6] ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=PI5656-1; Sequence=Displayed;
 CC Name=Short; Synonym=FGF-5;
 CC IsoId=PI5656-2; Sequence=VSP 001520, VSP 001521;
 CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, M30643; AA96698.1; -; mRNA.
 CC EMBL, M37823; AA802660.1; -; Genomic DNA.
 CC EMBL, M37821; AA802660.1; JOINED; Genomic DNA.
 CC EMBL, M37822; AA802660.1; JOINED; Genomic DNA.
 CC EMBL, M37821; AA802659.1; ALT_SEQ; Genomic DNA.
 CC EMBL, AB016516; BA33737.1; -; mRNA.
 CC EMBL, AK028694; BAC26069.1; -; mRNA.
 CC EMBL, AK028894; BAC26179.1; -; mRNA.
 CC EMBL, BC071227; AAH71227.1; -; mRNA.
 CC PIR, A36207; A36207.
 CC HSSP, P08620; 11J7.
 CC EMBL, EMBL000000029337; Mus musculus.
 CC MG1; MG1:95519; Fg5.
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0010001; P:glial cell differentiation; IMP.
 CC InterPro; IPR002209; GF heparin bd.
 CC InterPro; IPR002348; IL1_HBGF.
 CC Pfam; PF00167; FGF, 1.
 CC PRINTS; PR00263; HBGF_FGF.
 CC PRINTS; PR00262; IL1_HBGF.
 CC PRODOM; PD000831; IL1_HBGF, 1.
 CC PROSITE; PS00247; HBGF_FGF, 1.
 CC KW Alternative splicing; Glycoprotein; Growth factor; Mitogen;
 CC Proto-oncogene; Signal.
 CC FT SIGNAL 1 17 Potential.
 CC FT CHAIN 18 264 Fibroblast growth factor 5.
 CC FT COMBIDAS 53 59 Poly-Ser.
 CC FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
 CC FT VARSPPLIC 118 121 ILK1 -> QIV (in isoform Short).
 CC FT FTId=VSP 001520.
 CC FT VARSPPLIC 122 264 Missing (in isoform Short).
 CC FT FTId=VSP 001521.
 CC SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153BE923D1 CRC64;
 Query Match 33.6%; Score 90; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 4.7e-75;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 121 LEIPAVSOGIVGIRGVFNSKFLAMSKGKGLHSAKFTDDCKRFRFQNSYNTVSAATIR 180
 DB 119 LEIPAVSOGIVGIRGVFNSKFLAMSKGKGLHSAKFTDDCKRFRFQNSYNTVSAATIR 178
 QY 181 TKTGREYVALNKKKGAKRGCSPPVKKQH 210
 DB 179 TKTGREYVALNKKKGAKRGCSPPVKKQH 208
 RESULT 6
 FGFS RAT
 ID FGFS_RAT STANDARD; PRT; 266 AA.


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RESULT 12
Q8MN07_CANFA
ID Q8MN07_CANFA PRELIMINARY; PRT; 87 AA.
AC Q8MN07;
DT 01-MAR-2002 (TRMBLrel. 20, Created)
DT 01-MAR-2002 (TRMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 5 (fragment).
GN Name=FGF-5;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
NCBI_TaxID=9615;
OK NCB1_TaxID=9615;
RN
RP NUCLEOTIDE SEQUENCE.
RA Carwright J.M.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453760; AAL50825.1; -; Genomic_DNA.
DR HSSP; P08620; 11UT.
DR Ensemble; ENSCAG000000885; Canis familiaris.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF_1; IL1_HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
FT NON_TER 1
FT 87
SQ SEQUENCE 87 AA; 8491 MW; 940B9B02538C38CF CRC64;

Query Match
Best Local Similarity 100.0%; Score 16; DB 2; Length 87;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 RVGIGFHLQIYPPDGKV 109
DB 72 RVGIGFHLQIYPPDGKV 87

RESULT 13
Q13543_YEAST
ID Q13543_YEAST PRELIMINARY; PRT; 109 AA.
AC Q13543;
DT 01-JAN-1998 (TRMBLrel. 05, Created)
DT 01-JAN-1998 (TRMBLrel. 05, Last sequence update)
DT 10-MAY-2005 (TRMBLrel. 30, Last annotation update)
DE YLR294CP (YLR294C).
GN OrderedLocNames=YLR294C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
OK NCB1_TaxID=4932;
RN
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L.W., Riles L., Albermann K., Ande B.,
RA Anorge W., Benes V., Brueckner M., Delius H., Dubois B.,
RA Duesterhoeft A., Entlan K.-D., Floeth M., Goffeau A., Hebling U.,
RA Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Klein K.,
RA Koetter P., Louis E.J., Messengy F., Mewes H.-W., Miosga T.,
RA Moestl D., Mueller-Auer S., Nenwich U., Obermayer B., Pitarvandi E.,
RA Pohl T.M., Portetle D., Pirnille B., Rechmann S., Rieger M.,
RA Rinde M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C.,
RA Schwarz S., Underwood A.P., Urrestazu L.A., Vandenbol M.,
RA Verheeselt P., Viereckels F., Voet M., Volckaert G., Voss H.,
RA Wandt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A.,
RA Hani J., Honelsel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
(2)
RA NUCLEOTIDE SEQUENCE.
RA Pauley A.;

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RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Cherry J.M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Marischky G., Rolfs A., Richardson A., Kane M., Bagui M., Taycher E.,
RA Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzalez L., Vasconcelos A.T., Simpson A., Kolchek R., Harlow E.,
RA Laber J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U17243; AAB67352.1; -; Genomic_DNA.
DR EMBL; AY558218; AAS56544.1; -; Genomic_DNA.
DR PIR; S69307; S69307.
DR InAct; O13543; -.
KW Complete proteome.
SQ SEQUENCE 109 AA; 13120 MW; 02E1B166CFC70BEC CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 2; Length 109;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLSPULLLF 11
DB 82 SLSPULLLF 91

RESULT 14
Q7Y0C1_ORYZA
ID Q7Y0C1_ORYZA PRELIMINARY; PRT; 349 AA.
AC Q7Y0C1;
DT 01-OCT-2003 (TRMBLrel. 25, Created)
DT 01-OCT-2003 (TRMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DE Putative DoF zinc finger protein.
GN Name=OSJNB0079815.26;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=39947;
OK NCB1_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L., Tsaltrin T., Kim M.M., Bera J.V., Jin S.S.,
RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC099043; AAF50963.1; -; Genomic_DNA.
DR Gramene; Q7Y0C1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR003851; ZnF_Dof.
DR Pfam; PF02701; ZF_Dof; 1.
DR PROSITE; PS01361; ZF_DOF_1; UNKNOWN_1.
DR PROSITE; PS00884; ZF_DOF_2; 1.
SQ SEQUENCE 349 AA; 35653 MW; 7C8BBF28AC6CAFDF8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 2; Length 349;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 57 SSASSSPAAS 66
 |||||
 DB 249 SSASSSPAAS 258

RESULT 15

OS4TY7_DICDI PRELIMINARY; PRT; 418 AA.
 ID OS4TY7_DICDI
 AC OS4TY7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE MAD8-box transcription factor.
 GN Name=orf1; ORFNames=DDBD214892;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxId=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugeng R., Berriman M., Song J., Olsen R., Szatranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Plicher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just B., Morio T., Kost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Salto T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Loulsged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomie W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
 RA "The genome of the social amoeba Dictyostelium discoideum.";
 RT Nature 0:0-0(2005).
 RL -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAF10100074; FAL66675.1; -; Genomic_DNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 418 AA; 47546 MW; 8C86042A75C82D8A CRC64;

Query Match 3.7%; Score 10; DB 2; Length 418;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 55 SSSASSSPA 64
 |||||
 DB 388 SSSASSSPA 397

Search completed: April 11, 2006, 03:36:41
 Job time : 74 secs

CC used, pref. FGF-1 (AAR70812), EGF-5 (AAR70813), FGF-7 (AAR70814) or FGF-8
CC (AAR70815) mutants, in which at least 1 Cys residue is replaced by
CC conservative Ser substitutions. The fusion proteins are potent cytochalasin
CC agents to cells bearing the FGF receptor. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 268 AA;

SQ Sequence 268 AA;

Query Match	100.0%	Score 268	DB 2	Length 268
Best Local Similarity	100.0%	Pred. No. 8.6e-250		
Matches 268; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

Qy	1	MSLSLLLPFHLLITSAWAHGEKRLAPGQPEPATDRNPDISSSRQSSSSAMSSSSAS	60
Db	1	MSLSLLLPFHLLITSAWAHGEKRLAPGQPEPATDRNPDISSSRQSSSSAMSSSSAS	60
Qy	61	SSPAASLGSQSGLEQSSFWQSPSGRRTGSLYCRVIGFHLQIYDPQKVGSHBANLSTV	120
Db	61	SSPAASLGSQSGLEQSSFWQSPSGRRTGSLYCRVIGFHLQIYDPQKVGSHBANLSTV	120
Qy	121	LEIFAVSGQIVGIRGVFSNKKFLAMGKKGLHSAKTTDCKKFERQENSYNNTYASAIHR	180
Db	121	LEIFAVSGQIVGIRGVFSNKKFLAMGKKGLHSAKTTDCKKFERQENSYNNTYASAIHR	180
Qy	181	TEKTRBWWVVALNKGSGKARGCSPRVYKPOHISTHFLPRFKQSQPELSFTVTVPEKANPP	240
Db	181	TEKTRBWWVVALNKGSGKARGCSPRVYKPOHISTHFLPRFKQSQPELSFTVTVPEKANPP	240
Qy	241	SPIKSKIPLSAPRKQNTSVYKRLKPRFG	268
Db	241	SPIKSKIPLSAPRKQNTSVYKRLKPRFG	268

RESULT 2

AA80780 standard; protein; 268 AA.

AC AAR80780;

DT 13-MAY-1996 (first entry)

DE Fibroblast growth factor 5, FGF-5.

KM Conjugate; fibroblast growth factor; FGF; cytotoxin; saporin; eye;
KM cell proliferation; regulation; pterygia; corneal clouding; cancer;
KM psoriasis; rheumatoid arthritis.

OS Homo sapiens.

PN W09524928-A2.

PD 21-SEP-1995

PF 15-MAR-1995; 95WO-US003448.

PR 15-MAR-1994; 94US-00213446.

XX

XX

XX

XX

PT New conjugates of growth factor receptor ligand and targeted agent -
PT partic. DNA or cytochrome, used to control cell proliferation in the eye
PT e.g. to prevent growth of pterygi and corneal clouding.
XX
PS Claim 33; Page 144; 204APD; English.

PS Claim 33; Page 144; 204pp; English.

CC AAR80776-84 are fibroblast growth factors (FGF). FGF-1 to FGF-9
CC respectively. DNA encoding these fibroblast growth factors can be used to
CC create an FGF/saporin fusion protein. DNA encoding such fusion proteins

are useful for targeting saprolin (a cytotoxin) to a cell carrying the PGR receptor. Targeted agents (TA) other than saprolin which may be used include in partic. DNA encoding a therapeutic protein, antisense DNA or other cytotoxic agent. The linker sequence within the fusion protein may increase serum stability or intracellular availability of the TA. The conjugates of the invention are used to inhibit cell proliferation in cells carrying the particular growth factor receptor; also when TA is DNA it can be used to deliver this to cells (for gene therapy). A specific application is to prevent excessive proliferation of epithelial cells, fibroblasts and keratinocytes in the anterior eye after surgery, partic. to prevent recurrence of pterygii after surgical removal, closure of trabeculectomy after glaucoma surgery and corneal clouding after excimer laser treatment. Other conditions which may be treated include tumours, rheumatism, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis

Sequence 268 AA:

Query Match	100.0%	Score 268;	DB 2;	Length 268;
Best Local Similarity	100.0%	Pred. No. 8,6e-250;		
Matches 268: Conservative	0:	Mismatches	0:	Gaps 0

QY	1	MSLSFLLLFPSHLLISMAHGEKRLAPKGGGPAATDNPILGSSSRSSSSAMSSSSAS	60
Db	1	MSLSFLLLFPSHLLISMAHGEKRLAPKGGGPAATDNPILGSSSRSSSSAMSSSSAS	60
QY	61	SSPAASLQSGSGLEQSSFPQSPSGRRITSLYCRVQIGFHLQIYPFGKNGSHSAMLAV	120
Db	61	SSPAASLQSGSGLEQSSFPQSPSGRRITSLYCRVQIGFHLQIYPFGKNGSHSAMLAV	120
QY	121	LEIFAVSGQIVIGIRGVFSPKFLAMSKGKGLHSAKFTDDCKRERFOENSINTYASAIR	180
Db	121	LEIFAVSGQIVIGIRGVFSPKFLAMSKGKGLHSAKFTDDCKRERFOENSINTYASAIR	180
QY	161	TEKTRERWYVALNKGKAKAGCSPRVKPHISTHFLPRKQSEQPELSFTVYPEKKNIP	240
Db	161	TEKTRERWYVALNKGKAKAGCSPRVKPHISTHFLPRKQSEQPELSFTVYPEKKNIP	240
QY	241	SPIKSKIPISAPRKNTNSVYKRLKFRFG	268
Db	241	SPIKSKIPISAPRKNTNSVYKRLKFRFG	268

RESULT 3

ID AAW75715 standard; protein; 268 AA.

AAW75715; AC

DT 07-DEC-1998 (first entry)

DE Fibroblast growth factor-5.

KW Fibroblast growth factor-5; FGF-5; mutetin; protein engineering; heparin;

XX

XX

FT Misc-differen

(Claim 3), preferably Ala, Phe, Ser, Gly, Met, Leu or

FT Misc-difference 164

FT (Claim 7), preferably Ala, Gly or Ser"

FT /note= "Asn-169 may be replaced by another amino acid

FT Tyr, especially Ala, Gly or Ser"
XX W09839436-A2.
XX
XX 11-SEP-1998.
XX
XX 03-MAR-1998; 98WO-JP000878.
XX
XX 03-MAR-1997; 97US-0040785P.
XX
XX (EISA) EISAI CO LTD.
XX
XX Zhu H, Kalyanaraman R, Kawai T;
XX WPI: 1998-495843/42.
XX
XX Fibroblast growth factor mutein and DNA - having reduced receptor binding
PT and able to bind heparin, useful for treating and regulating heparin-
PT related disorders e.g. thrombosis.
XX
XX
XX Disclosure; Page 55-56; 71pp; English.
XX
XX This is the amino acid sequence of fibroblast growth factor-5 (FGF-5).
CC Claimed DNA molecules of the invention encode FGF mutein polypeptides
CC (see AAW75711-20) that show reduced FGF receptor binding activity but
CC which retain the ability to bind heparin. For FGF-5, amino acid residues
CC 162, 169 and 172 are preferably replaced by other amino acid residues,
CC with an optional further replacement of the Glu-164 residue. The mutein
CC may be further modified by replacement of the Cys residues to reduce
CC aggregation. The mutein is obtained by site-specific or site-directed
CC mutagenesis of FGF-5 DNA, incorporation of the mutated DNA into a vector
CC and expression in host cells. The FGF muteins are used to treat heparin-
CC related disorders, such as excessive bleeding induced by heparin,
CC opthamatic disorders and heparin-associated thrombocytopenia and
CC thrombosis. They may also be used for drug design
XX
XX Sequence 268 AA;
SQ
Query Match 100.0%; Score 268; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.6e-250;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW PRO533; FGF-19; fibroblast growth factor; human; diagnosis; treatment;
KW tumour; neoplastic cell growth; cell proliferation; tumorigenesis; cancer;
KW autocrine signalling; FGF-5.
XX
XX Homo sapiens.
XX
XX W09927100-A1.
XX
XX 03-JUN-1999.
XX
XX 25-NOV-1998; 98WO-US025190.
XX
XX 25-NOV-1997; 97US-0066840P.
XX 21-SEP-1998; 98US-00158342.
XX
XX (GENTH) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;
XX WPI: 1999-347718/29.
XX
XX Nucleic acid encoding fibroblast growth factor - 19, useful for the
PT diagnosis, prevention and treatment of cancers.
XX
XX Disclosure; Fig 11; 88pp; English.
XX
XX This invention describes a novel human fibroblast growth factor, PRO533,
CC also known as fibroblast growth factor-19 (FGF-19). The nucleic acids,
CC methods and PRO533 polypeptides disclosed may be used in the diagnosis
CC and treatment of tumour and/or conditions characterized by modulation of
CC PRO533 expression, or in the preparation of compositions for such
CC therapies. These compositions and methods may be used in the diagnosis
CC and treatment of neoplastic cell growth and proliferation in mammals
CC (especially humans). The invention is based on the identification of
CC genes that are amplified in the genome of tumour cells. Such gene
CC amplification is expected to be associated with the over expression of
CC the gene product and contribute to tumourgenesis and/or autocrine
CC signalling. Accordingly, the proteins encoded by the amplified genes are
CC believed to be useful targets for the diagnosis and/or treatment of
CC certain cancers and may act as predictors of the prognosis for tumour
CC treatments
XX
XX Sequence 268 AA;
SQ
Query Match 100.0%; Score 268; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.6e-250;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
AAV08585
ID AAY08585 standard; protein; 268 AA.
XX
XX AAY08585;
XX
XX 05-AUG-1999 (first entry)
XX
XX Human FGF-5 protein fragment.
XX

RESULT 5
AAV32337
ID AAY32337 standard; protein; 268 AA.
XX

AC	AA32337,
XX	
DT	28-FEB-2000 (first entry)
XX	
DE	Human fibroblast growth factor 5.
XX	
KW	Fibroblast growth factor 5; FGF-5; human; mutein; vascular disorder;
KW	smooth muscle cell proliferation; rheumatoid arthritis; tumour;
KW	angiogenesis; Kaposi's sarcoma; restenosis; ophthalmic disorder;
KW	psoriasis; coagulant; heparin; thrombosis; thrombocytopenia.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Misc-difference 156
FT	/note= "replaced with another amino acid in claimed
FT	mutcin of Claim 5"
FT	Misc-difference 161
FT	/note= "replaced with another amino acid in claimed
FT	mutcin of Claim 7"
FT	Misc-difference 214
FT	/note= "replaced with another amino acid in claimed
FT	mutcin of Claim 1"
XX	
PN	WO9955861-A2.
XX	
PD	04-NOV-1999.
XX	
PE	15-APR-1999; 99WO-JP002013.
XX	
PR	28-APR-1998; 98US-00067929.
XX	
PA	(EISA) EISAI CO LTD.
XX	
PI	Zhu H, Kalyanaraman R;
DR	WPI: 2000-062030/05.
XX	
PT	New polynucleotides encoding fibroblast growth factor muteins used for
PT	treatment of ophthalmic disorders, tumorigenic disorders and restenosis.
XX	
PS	Claim 1; Page 81-82; 93pp; English.
XX	
CC	This sequence represents human fibroblast growth factor 5 (FGF-5). The
CC	invention relates to isolated nucleic acids encoding FGF mutcin
CC	polypeptides. FGF muteins that exhibit increased binding affinity for FGF
CC	receptors and reduced mitogenic activity are provided. Such muteins have
CC	amino acid replacements at positions corresponding to position 138 (claim
CC	1) of FGF-2 (see AA32334). They can be used to prevent or inhibit the
CC	undesired growth and proliferation of FGF-responsive cells. Such cells
CC	occur in vascular disorders characterised by accelerated smooth muscle
CC	cell proliferation, such as rheumatoid arthritis, tumour angiogenesis,
CC	Kaposi's sarcoma, restenosis, in-stent restenosis, certain ophthalmic
CC	disorders and dermatological disorders, such as psoriasis. Also provided
CC	are FGF muteins that exhibit reduced receptor binding activity, but
CC	retain the ability to bind heparin. These muteins have amino acid
CC	replacements corresponding to positions 88 (claim 5) and 93 (claim 7) and
CC	optionally position 96 of FGF-2. They can be used as coagulants for
CC	heparin-associated bleeding, antagonists of heparin-induced angiogenesis,
CC	and for treating heparin-induced thrombocytopenia and thrombosis. In
CC	preferred muteins, the native FGF amino acid is replaced by Ala, Phe,
CC	Gly, Ser, Met or Tyr, especially Ala, Gly or Ser, and particularly Ala.
CC	Cys residues may also be substituted to reduced polypeptide aggregation
XX	
SQ	Sequence 268 AA:
Query Match	100.0%; Score 268; DB 3; Length 268;
Best Local Similarity	100.0%; Pred. No. 8.6e-250;
Matches 268; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

```

1 MSLSLLILFFSHLILSMAHAGEKRLAPGCGEPATDNPITGSSRSSSSAMSSSNAS 60
1 MSLSLLILFFSHLILSMAHGEKRLAPGCGEPATDNPITGSSRSSSSAMSSSNAS 60

```

Qy	61	SSPAAALSGSGSGLEQSSSPQSPSPRRFRGSLYCVGVGFGHQLQTPDQKNGSHRAANLSTV	120
Db	61	SSPAAALSGSGSGLEQSSSPQSPSPRRFRGSLYCVGVGFGHQLQTPDQKNGSHRAANLSTV	120
Qy	121	LEIFPAVSQSIIVGIRGVFSNKFPLAMSKKCLHASAKFTDCCFRERFOENSYNTYASAIHR	180
Db	121	LEIFPAVSQSIIVGIRGVFSNKFPLAMSKKCLHASAKFTDCCFRERFOENSYNTYASAIHR	180
Qy	181	TEXTGSEWYVALNKGKAVRGCGSPVVKQHISTHFLPFRKQSEQPELSFTVTVPEKKNPP	240
Db	181	TEXTGSEWYVALNKGKAVRGCGSPVVKQHISTHFLPFRKQSEQPELSFTVTVPEKKNPP	240
Qy	241	SPISKRIPLSAPRKNTNSVQVTLKGRFG	268
Db	241	SPISKRIPLSAPRKNTNSVQVTLKGRFG	268
RESULT 6			
AAAY90414			
XX	AAAY90414	standard; protein; 268 AA.	
AC			
XX	AAAY90414;		
XX			
DT	18-JUL-2000	(first entry)	
DE			
XX	FGF-5, SEQ ID NO:14.		
XX			
KM	Targetted gene delivery; fibroblast growth factor receptor;		
KM	FGFR-binding protein; FGF-2; bFGF; nucleic acid binding protein;		
KM	receptor-internalised ligand; cyclooxin; seporin; gene therapy; cytocide;		
KM	antiproliferative; cancer; melanoma; diabetic retinopathy;		
KM	rheumatoid arthritis; restenosis; Dupuytren's contracture; psoriasis;		
KM	eczema.		
XX			
OS	Unidentified.		
XX			
PN	US6037329-A.		
PD			
XX	14-MAR-2000.		
PF			
XX	24-SEP-1996;	96US-00718904.	
XX			
PR	15-MAR-1994;	94US-00213446.	
PR	15-MAR-1994;	94US-00213447.	
PR	29-AUG-1994;	94US-00297961.	
PR	13-SEP-1994;	94US-00305771.	
PR	16-MAY-1995;	95US-00441979.	
XX			
PA	(SELE-) SELECTIVE GENETICS INC.		
PI			
XX	Chandler LA, Sosnowski BA, Baird JA;		
DR			
XX	WPI; 2000-292008/25.		
XX			
PT	Gene delivery system, useful for treating or preventing cancer and		
PT	rheumatoid arthritis, comprises receptor-internalized ligand linked to		
PT	nucleic acid binding domain and nucleic acid.		
XX			
XX			
PS	Claim 25; Col 103-104; 131p; English.		
XX			
CC	The invention relates to a novel gene delivery composition for the		
CC	targetted delivery of cyclooxins or prodn-converting enzymes to		
CC	proliferating cells. The gene delivery composition comprises a protein		
CC	that binds the fibroblast growth factor receptor (FGFR) which is fused orn		
CC	chemically conjugated to a nucleic acid binding domain. The nucleic acid		
CC	binding domain is complexed with a suitable expression construct encoding		
CC	a cytotoxin such as seporin. One or more linkers may join the FGFR-		
CC	binding protein to the nucleic acid binding protein. These are selected		
CC	to increase the specificity, toxicity, solubility, serum stability or		
CC	intracellular availability, and may serve to promote condensation of		
CC	nucleic acids for delivery to a cell. The fusion protein binds to FGFR		
CC	and is internalised by cells that carry this receptor. The gene delivery		

CC composition is used for the therapeutic alteration of the function, gene
CC expression and viability of cells. In particular, it may be used for the
CC treatment and prevention of cell proliferative disorders, for example
CC after eye surgery, melanoma and many other sorts of cancer, rheumatoid
CC arthritis, restenosis, Dupuytren's contracture, diabetic retinopathy,
CC psoriasis and eczema. The gene delivery compositions of the invention
CC have high specificity for particular cells and can deliver larger amounts
CC of DNA compared to prior art methods. Sequences AA90410-AA90418
CC represent members of the fibroblast growth factor (FGF) family of
CC proteins. AA90448 represents wild-type human FGF-2 (basic FGF, bFGF)
CC which is encoded by AAI12868. AAI12897-AI2900 encode the human FGF-2
CC mutants AA90461-Y90464, and AA90465-Y90466 represent additional human
CC FGF-2 mutants used in the invention. AA90450 represents a mutagenised
CC FGF C-terminus
XX
SQ Sequence 268 AA;
Query Match 100.0%; Score 268; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.6e-250;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLILFSPSHLILSAMAHGKRLAPKGPAPATDRNPIGSSSRQSSSAMSSSAS 60
DB 1 MSLSFLLILFSPSHLILSAMAHGKRLAPKGPAPATDRNPIGSSSRQSSSAMSSSAS 60
QY 61 SSPASISLQSGSGLEQSSFPQSPSGRRGSLYCRVGIGFHLQIYPDGKNSHEANMLSV 120
DB 61 SSPASISLQSGSGLEQSSFPQSPSGRRGSLYCRVGIGFHLQIYPDGKNSHEANMLSV 120
QY 121 LEIFAVSQGIIVGIRGVFNKFLAMSKKGLASAKFTDDCKFRERFQENSNTYTAIAHR 180
DB 121 LEIFAVSQGIIVGIRGVFNKFLAMSKKGLASAKFTDDCKFRERFQENSNTYTAIAHR 180
QY 181 TEKTRBMYVALNKGKAKRGCSPRVKPQHISTHLPFRKQSEQBELSFTVTVPKKNP 240
DB 181 TEKTRBMYVALNKGKAKRGCSPRVKPQHISTHLPFRKQSEQBELSFTVTVPKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
RESULT 7
AAE00636 standard; protein; 268 AA.
AC AAE00636;
DT 02-JUL-2001 (first entry)
DE Human MUSGF5A protein of second open reading frame.
XX
XX Human; fibroblast growth factor-5; FGF-5; neoplasm; cytostatic; RCC;
KW renal cell carcinoma; immunomodulator; gene therapy; carcinoma; breast;
KW prostate; bladder; pancreas; TAA; tumour associated antigen; MUSGF-5A;
KW horseshoe kidney; Hippel-Lindau disease; acquired renal cystic disease;
KW adult polycystic kidney disease.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX FT Region 161..220
XX FT /label= Immunogenic_epitope
XX PN WO200125271-A2.
XX PD 12-APR-2001.
XX PF 29-SEP-2000; 2000MO-US026689.
XX PR 02-OCT-1999; 99US-0157103P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Hanada K, Yang JC;
XX WPI, 2001-290607/30.
DR N-PSDB; AAD03934.
XX
PT Treating a subject having a neoplasm expressing fibroblast growth factor-
PT 5 (FGF-5), e.g. prostate, breast, bladder, or pancreas carcinoma,
PT comprises modulating an immune response to FGF-5 or modulating FGF-5
PT expression or activity.
XX
PS Claim 7; Page 87-88; 101pp; English.
XX
CC The present invention relates to a method for treating a subject having
CC neoplasm expressing fibroblast growth factor-5 (FGF-5) comprises
CC modulating an immune response to FGF-5 or FGF-5 expression or activity.
CC FGF is a tumour associated antigen (TAA). The method is useful for
CC treating or preventing a neoplasm such as prostate carcinoma, breast
CC carcinoma, bladder carcinoma, pancreas carcinoma, and renal cell
CC carcinoma (RCC) and diseases such as Hippel-Lindau disease, horseshoe
CC kidney, adult polycystic kidney disease and acquired renal cystic
CC disease. FGF-5 polypeptides may be used as immunogen in the production of
CC antibodies, which are useful in quantitative immunoassays that determine
CC concentrations of antigen-bearing substances in biological samples, and
CC to (semi-)quantitatively identify the presence of antigen in a biological
CC sample. The antibodies may also be used to treat FGF-5-expressing or
CC overexpressing tumours by decreasing FGF-5 activity, as diagnostic agents
CC to monitor the progression or regression of an FGF-5-expressing or
CC overexpressing tumour in a patient undergoing therapy for the treatment
CC of neoplasm. FGF-5 cDNA is also useful in gene therapy. The present
CC sequence is a protein encoded by the second open reading frame of human
CC MUSGF-5A cDNA
XX
SQ Sequence 268 AA;
Query Match 100.0%; Score 268; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.6e-250;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLILFSPSHLILSAMAHGKRLAPKGPAPATDRNPIGSSSRQSSSAMSSSAS 60
DB 1 MSLSFLLILFSPSHLILSAMAHGKRLAPKGPAPATDRNPIGSSSRQSSSAMSSSAS 60
QY 61 SSPASISLQSGSGLEQSSFPQSPSGRRGSLYCRVGIGFHLQIYPDGKNSHEANMLSV 120
DB 61 SSPASISLQSGSGLEQSSFPQSPSGRRGSLYCRVGIGFHLQIYPDGKNSHEANMLSV 120
QY 121 LEIFAVSQGIIVGIRGVFNKFLAMSKKGLASAKFTDDCKFRERFQENSNTYTAIAHR 180
DB 121 LEIFAVSQGIIVGIRGVFNKFLAMSKKGLASAKFTDDCKFRERFQENSNTYTAIAHR 180
QY 181 TEKTRBMYVALNKGKAKRGCSPRVKPQHISTHLPFRKQSEQBELSFTVTVPKKNP 240
DB 181 TEKTRBMYVALNKGKAKRGCSPRVKPQHISTHLPFRKQSEQBELSFTVTVPKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
RESULT 8
AAE04405 standard; protein; 268 AA.
AC AAE04405;
DT 04-SEP-2001 (first entry)
DE Human fibroblast growth factor-5 (FGF-5).
XX
XX Human; zFGF10; fibroblast growth factor-5; FGF-5; antiatherosclerotic;
KW vasotrophic; anorectic; antipsoriatic; antidiabetic; cerebroprotective;
KW cytostatic; vulnerary; diabetes mellitus; amyotrophic lateral sclerosis;

KW therapy; cerebrovascular stroke; neuropathy; angiogenesis; wound healing;
 KW revascularisation; diabetic foot ulcer; stroke; coronary reperfusion;
 KW ischaemia; hypertension; psoriasis; neuroblastoma; glioblastoma;
 KW carcinoma; prostatic hypertrophy.

OS Homo sapiens.

PN WO200147957-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000MO-US035581.

PR 29-DEC-1999; 99US-00474279.

PA (Zymo) ZYMOGENETICS INC.

PI Conklin DC;

DR WPI; 2001-418223/44.

PT Novel fibroblast growth factor homolog, zFGF10, useful for treating
 PT psoriasis, stimulating proliferation of mesenchymal cells, keratinocytes
 PT in culture, promoting wound healing of epidermis, improving cardiac
 PT function.

PS Disclosure; Page 59-60; 62pp; English.

XX The present sequence is fibroblast growth factor-5 (FGF-5) from human.
 CC This protein is a member of the FGF family. The present invention relates
 CC to novel human zFGF10 protein and its DNA. zFGF-10 is a homologue of
 CC fibroblast growth factor (FGF). The zFGF10 sequences and their antibodies
 CC are useful for identifying and isolating neuronal, prostatic and
 CC pancreatic cell proliferation. They are used in the treatment of
 CC disorders associated with diabetes mellitus, neural cell development or
 CC degeneration, amyotrophic lateral sclerosis, cerebro-vascular stroke,
 CC neuropathy associated with lack of maintenance of neuronal
 CC differentiation, and congenital disorders of the nervous system or lack
 CC of neuronal development. zFGF-10 sequences are used for promoting
 CC angiogenesis and wound healing, for revascularisation in the eye, for
 CC complications related to poor circulation such as diabetic foot ulcers,
 CC for stroke, following coronary reperfusion and for improving cardiac
 CC function. They are used to protect and promote the recovery of the
 CC epithelial cells in the gastrointestinal tract, small intestine and oral
 CC mucosa after treatment with chemotherapy and/or radiation and to reduce
 CC damage to the tissues caused by ischaemia or ischaemia-reperfusion
 CC events, particularly in the heart or brain. They are also used for the
 CC induction of skeletal muscle neogenesis and/or hyperplasia, kidney
 CC regeneration and/or for treatment of systemic and pulmonary hypertension.
 CC zFGF-10 proteins are used for stimulating proliferation of mesenchymal
 CC cells, epidermal cells or keratinocytes. The zFGF-10 antagonists are used
 CC to treat psoriasis associated with keratinocyte. zFGF-10 binding proteins
 CC are useful for treating neuroblastoma, glioblastoma, prostatic
 CC hypertrophy, prostatic carcinoma and pancreatic carcinoma

CC Sequence 268 AA;

Query Match 100.0%; Score 268; DB 4; Length 268;
 Best Local Similarity 100.0%; Pred. No. 8.6e-250; Indels 0; Gaps 0;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFPFSLILTSAMAHGEKRLAPKQGPATDNPISGSSROSSSSAMSSSSAS 60
 DB 1 MSLSFLLLFPFSLILTSAMAHGEKRLAPKQGPATDNPISGSSROSSSSAMSSSSAS 60
 QY 61 SSPAASLSGSGGLEQSSFFQWSPSGRRTGSLYCRVIGIFHLQIYDPGKVGSHANMLSV 120
 DB 61 SSPAASLSGSGGLEQSSFFQWSPSGRRTGSLYCRVIGIFHLQIYDPGKVGSHANMLSV 120
 QY 121 LEIFAVSOGIIVGIRGVFNKFLAMSKKGLHASAKFTDDCKRERFOENSYTYVASAIHR 180
 DB 121 LEIFAVSOGIIVGIRGVFNKFLAMSKKGLHASAKFTDDCKRERFOENSYTYVASAIHR 180
 QY 121 LEIFAVSOGIIVGIRGVFNKFLAMSKKGLHASAKFTDDCKRERFOENSYTYVASAIHR 180
 DB 121 LEIFAVSOGIIVGIRGVFNKFLAMSKKGLHASAKFTDDCKRERFOENSYTYVASAIHR 180

QY 181 TEKTRBMYVALNKRKAKRGCSPRVKPOHISTHPLRPFKQSEOPBELSFTYVPEKKNP 240
 DB 181 TEKTRBMYVALNKRKAKRGCSPRVKPOHISTHPLRPFKQSEOPBELSFTYVPEKKNP 240
 QY 241 SPIKSKIPLSAPRKYTNVSKYRLKFRFG 268
 DB 241 SPIKSKIPLSAPRKYTNVSKYRLKFRFG 268

RESULT 9

AAB50701
 ID AAB50701 standard; protein, 268 AA.

AC AAB50701;

DT 20-MAR-2001 (first entry)

DE Human fibroblast growth factor 5 SEQ ID NO: 11.

KW Human; fibroblast growth factor 11; FGF-11; cancer; autoimmune disorder;
 KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
 KW wound healing; neurological disease; infection.

OS Homo sapiens.

PN WO200071715-A1.

PD 30-NOV-2000.

PF 16-MAY-2000; 2000MO-US013331.

PR 21-MAY-1999; 99US-0135524P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Alderson R, Meider R, Duan RD, Hu J;

DR WPI; 2001-016408/02.

PT Polynucleotide encoding human fibroblast growth factor 11, useful in the
 PT diagnosis, treatment and prevention of cancer, immune disorders,
 PT cardiovascular disorders and neurological diseases.

PS Disclosure; Page 243-244; 250pp; English.

CC The present invention provides the protein and coding sequences for human
 CC fibroblast growth factor 11 (FGF-11). These sequences can be used in the
 CC diagnosis and treatment of infections, cancer, autoimmune disorders,
 CC hyperproliferative disorders, cardiovascular disorders and neurological
 CC diseases, to prevent angiogenesis and to aid wound healing

CC Sequence 268 AA;

Query Match 100.0%; Score 268; DB 4; Length 268;
 Best Local Similarity 100.0%; Pred. No. 8.6e-250; Indels 0; Gaps 0;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLLFPFSLILTSAMAHGEKRLAPKQGPATDNPISGSSROSSSSAMSSSSAS 60
 DB 1 MSLSFLLLFPFSLILTSAMAHGEKRLAPKQGPATDNPISGSSROSSSSAMSSSSAS 60
 QY 61 SSPAASLSGSGGLEQSSFFQWSPSGRRTGSLYCRVIGIFHLQIYDPGKVGSHANMLSV 120
 DB 61 SSPAASLSGSGGLEQSSFFQWSPSGRRTGSLYCRVIGIFHLQIYDPGKVGSHANMLSV 120
 QY 121 LEIFAVSOGIIVGIRGVFNKFLAMSKKGLHASAKFTDDCKRERFOENSYTYVASAIHR 180
 DB 121 LEIFAVSOGIIVGIRGVFNKFLAMSKKGLHASAKFTDDCKRERFOENSYTYVASAIHR 180
 QY 181 TEKTRBMYVALNKRKAKRGCSPRVKPOHISTHPLRPFKQSEOPBELSFTYVPEKKNP 240
 DB 181 TEKTRBMYVALNKRKAKRGCSPRVKPOHISTHPLRPFKQSEOPBELSFTYVPEKKNP 240

QY 241 SPIKSIPLSAPRKNTNSVKYRLKFRFG 268
 |||||
 DB 241 SPIKSIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 10

AAB85816
 ID AAB85816 standard; protein; 268 AA.

AC AAB85816;

DT 29-OCT-2001 (first entry)

DE Human fibroblast growth factor (FGF)-5.

KW Fibroblast growth factor; FGF; FGF-23; osteopathic; vulnery; ADHR;
 KW hepatocytic; autosomal dominant hypophosphatemic rickets; human;
 KW anglogenesis; gene-therapy; liver disorder; antisense-therapy.

OS Homo sapiens.

PN WO200161007-A2.

PD 23-AUG-2001.

PF 15-FEB-2001; 2001WO-US004778.

PR 15-FEB-2000; 2000US-0182442P.

PR 20-APR-2000; 2000US-0198903P.

PR 15-FEB-2001; 2001US-00784581.

PA (AMGE-) AMGEN INC.

PI Luethy R, Yang R, Sugas S, Sarosi D;

DR WPI; 2001-514774/56.

PT An isolated nucleic acid molecule encoding a fibroblast growth factor 23
 useful for treating autosomal dominant hypophosphatemic rickets.

PS Example 1; Fig 2A-G; 158pp; English.

CC The invention provides a human fibroblast growth factor (FGF)-23
 CC polypeptide. The encoding DNA insert is contained in ATCC Deposit No. PMA
 CC -1617. FGF-23 can be expressed by standard recombinant methodology. The
 CC FGF-23 polypeptides, polynucleotides, modulators and antibodies are
 CC useful for treating, preventing, or ameliorating an FGF-23 polypeptide-
 CC related disease, condition or disorder especially autosomal dominant
 CC hypophosphatemic rickets (ADHR). They are also useful for diagnosing a
 CC pathological condition and for stimulating angiogenesis, promoting wound
 CC healing and treating disorders of the liver. Sequences AAB85812-29
 CC represent human FGF protein sequences used for comparison studies with
 CC FGF-23

CC Sequence 268 AA;

Query Match 100.0%; Score 268; DB 4; Length 268;
 Best Local Similarity 100.0%; Pred. No. 8, 6e-250;

Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSFLLILFFSHLILSAMHGERKLA PKQPGPAADRNPICSSSSQSSSSAMSSSSAS 60

DB 1 MSLSFLLILFFSHLILSAMHGERKLA PKQPGPAADRNPICSSSSQSSSSAMSSSSAS 60

QY 61 SSPAASISGSGSGLEOSSPQWSPSGRTGSLVCRVGIGFHLQIYPPDGKWNQSHRANLTV 120

DB 61 SSPAASISGSGSGLEOSSPQWSPSGRTGSLVCRVGIGFHLQIYPPDGKWNQSHRANLTV 120

QY 121 LBIFAVSQGIVGIRGVSNKFLAMSKKGLHASKFTDDCKFRFRFQENSNTYASAIHR 180

DB 121 LBIFAVSQGIVGIRGVSNKFLAMSKKGLHASKFTDDCKFRFRFQENSNTYASAIHR 180

QY 181 TEKTRWYVALNKGAKGCGSPRVAPQHI STHFLFRKQSEQPELSFTVTVPEKNPP 240

DB 181 TEKTRWYVALNKGAKGCGSPRVAPQHI STHFLFRKQSEQPELSFTVTVPEKNPP 240
 |||||
 QY 241 SPIKSIPLSAPRKNTNSVKYRLKFRFG 268
 |||||
 DB 241 SPIKSIPLSAPRKNTNSVKYRLKFRFG 268

RESULT 11

ADG34580
 ID ADG34580 standard; protein; 268 AA.

AC ADG34580;

DT 18-DEC-2003 (first entry)

DE Human fibroblast growth factor 5 (FGF-5) protein.

KW Gene delivery; fibroblast growth factor; FGF; FGF receptor; gene therapy;
 KW hyperproliferative disorder; neoplastic disease; ligand;
 KW nucleic acid binding domain; NABD; cytochrome; therapeutic; produg;
 KW ribozyme; antisense; ribosome inactivating protein; seporin; gelonin;
 KW diapherix toxin; elongation factor 2; HSV thymidine kinase;
 KW cytosine deaminase; human; FGF-5.

OS Homo sapiens.

PN US6503886-B1.

PD 07-JAN-2003.

PF 24-NOV-1999; 99US-00449249.

PR 15-MAR-1994; 94US-00213446.

PR 15-MAR-1994; 94US-00213447.

PR 29-AUG-1994; 94US-00297961.

PR 13-SEP-1994; 94US-00305771.

PR 16-MAY-1995; 95US-00441979.

PR 24-SEP-1996; 96US-00718904.

PA (SELE-) SELECTIVE GENETICS INC.

PI Baird UA, Chandler LA, Sosnowski BA;

DR WPI; 2003-361554/34.

PT Gene delivery composition for therapeutic treatments, comprises

PT polypeptide that binds to fibroblast growth factor receptor-nucleic acid

PT molecule.

PS Claim 14; SEQ ID NO 14; 130pp; English.

CC The invention discloses a gene delivery composition comprising a
 CC polypeptide that binds to a fibroblast growth factor (FGF) receptor-
 CC nucleic acid molecule. The nucleic acid molecule is chemically conjugated
 CC or fused to the polypeptide that binds to an FGF receptor. The delivery
 CC composition binds to an FGF receptor and is internalized specifically in
 CC cells bearing the FGF receptor. The invention relates to the treatment
 CC (e.g. gene therapy) of diseases (e.g. hyperproliferative disorders and
 CC neoplastic diseases) and, more specifically, to the preparation and use
 CC of complexes containing receptor-binding internalized ligands, nucleic
 CC acid binding domain (NABD) and cytochrome-encoding agents to alter the
 CC function, gene expression or viability of a cell in a therapeutic manner.
 CC The nucleic acid molecule is a produg-encoding agent, a ribozyme or an
 CC antisense molecule. The cytochrome-encoding agent encodes a ribosome
 CC inactivating protein, preferably a seporin, gelonin or diapherix toxin.
 CC It also encodes its elongation factor 2 and further comprises a tissue-
 CC specific promoter operably linked to the molecule. The produg-encoding
 CC agent encodes HSV thymidine kinase or cytosine deaminase. The polypeptide
 CC that binds to an FGF receptor can be FGF-1 polypeptide, FGF-2
 CC polypeptide, FGF-3 polypeptide, FGF-4 polypeptide, FGF-5 polypeptide, FGF
 CC -6 polypeptide, FGF-7 polypeptide, FGF-8 polypeptide or FGF-9
 CC polypeptide. The invented composition has increased specificity and

CC delivers higher amounts of nucleic acids to targeted cells. The sequence
CC presented is the human FGF-5 protein.

XX Sequence 268 AA;

Query Match 100.0%; Score 268; DB 7; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.6e-250;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MSLSTLLLFPSHLILSAMHGEKRLAPKGPAPATDRNPIGSSRSOSSSAMSSSSAS 60
   |||||||
DB 1 MSLSTLLLFPSHLILSAMHGEKRLAPKGPAPATDRNPIGSSRSOSSSAMSSSSAS 60
QY 61 SSPASISQSGSLQSSSFQWSPSGRRTSLYCRVIGIYDIPDGKNGSHEANMLSV 120
   |||||||
DB 61 SSPASISQSGSLQSSSFQWSPSGRRTSLYCRVIGIYDIPDGKNGSHEANMLSV 120
QY 121 LEIFAVSQIGVIGRVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSNTYASAIHR 180
   |||||||
DB 121 LEIFAVSQIGVIGRVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSNTYASAIHR 180
QY 181 TEKTRGEMVVALNKGAKRGCSPRVKPOHISTHFLPRKQSEBELSTYTVPEKKNP 240
   |||||||
DB 181 TEKTRGEMVVALNKGAKRGCSPRVKPOHISTHFLPRKQSEBELSTYTVPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
   |||||||
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
```

RESULT 12

ADH92004
ID ADH92004 standard; protein; 268 AA.

XX ADH92004;

DT 22-APR-2004 (first entry)

DE Fibroblast growth factor 5 (FGF-5) protein.

XX cytostatic; ophthalmological; gene therapy; human;
KW receptor-binding internalised ligand; nucleic acid binding domain;
KW cytoxicity-encoding agent; cell surface receptor; cell proliferation;
KW cancer; smooth muscle cell hyperplasia; fibroblast growth factor; FGF.

XX Unidentified.

XX US2003143217-A1.

PD 31-JUL-2003.

PF 02-JUL-2002; 2002US-00189360.

PR 15-MAR-1994; 94US-00213446.

PR 15-MAR-1994; 94US-00213447.

PR 29-AUG-1994; 94US-00297961.

PR 13-SEP-1994; 94US-00305771.

PR 16-MAY-1995; 95US-00441979.

PR 24-SEP-1996; 96US-00718904.

PR 24-NOV-1999; 99US-00449249.

XX (SELE-) SELECTIVE GENETICS INC.

PI Baird UA, Chandler LA, Sosnowski BA;

DR WPI; 2003-787221/74.

XX New pharmaceutical composition comprising receptor-binding internalized
PT ligand-nucleic acid binding domain-cytocine-encoding agent, useful for
PT preventing excessive cell proliferation in the eye or for treating e.g.
XX cancer.

PS Disclosure; SEQ ID NO 14; 137bp; English.

XX The invention describes a pharmaceutical composition comprising receptor-
CC binding internalised ligand-nucleic acid binding domain-cytocine-encoding
CC agent. The receptor-binding internalised ligand is a polypeptide reactive
CC with a cell surface receptor. The nucleic acid binding domain binds to a
CC nucleic acid and is chemically conjugated or fused to the receptor-
CC binding internalised ligand. The cytoxicity-encoding agent is a nucleic
CC acid molecule encoding a cytoxicity and is bound to the nucleic acid
CC binding domain. The receptor-binding internalised ligand-nucleic acid
CC binding domain-cytocine-encoding agent binds to the cell surface receptor
CC and internalises the cytoxicity-encoding agent in cells bearing the
CC receptor. The pharmaceutical composition is useful for preventing
CC excessive cell proliferation in the eye or for treating cancer or smooth
CC muscle cell hyperplasia. This is the amino acid sequence of a fibroblast
CC growth factor (FGF) that can be modified and used as a receptor binding
CC ligand of the invention.

XX Sequence 268 AA;

Query Match 100.0%; Score 268; DB 7; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.6e-250;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MSLSTLLLFPSHLILSAMHGEKRLAPKGPAPATDRNPIGSSRSOSSSAMSSSSAS 60
   |||||||
DB 1 MSLSTLLLFPSHLILSAMHGEKRLAPKGPAPATDRNPIGSSRSOSSSAMSSSSAS 60
QY 61 SSPASISQSGSLQSSSFQWSPSGRRTSLYCRVIGIYDIPDGKNGSHEANMLSV 120
   |||||||
DB 61 SSPASISQSGSLQSSSFQWSPSGRRTSLYCRVIGIYDIPDGKNGSHEANMLSV 120
QY 121 LEIFAVSQIGVIGRVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSNTYASAIHR 180
   |||||||
DB 121 LEIFAVSQIGVIGRVFNSKFLAMSKKGLHASAKFTDDCKRERFOENSNTYASAIHR 180
QY 181 TEKTRGEMVVALNKGAKRGCSPRVKPOHISTHFLPRKQSEBELSTYTVPEKKNP 240
   |||||||
DB 181 TEKTRGEMVVALNKGAKRGCSPRVKPOHISTHFLPRKQSEBELSTYTVPEKKNP 240
QY 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
   |||||||
DB 241 SPIKSKIPLSAPRKNTNSVKYRLKFRFG 268
```

RESULT 13

ADS20334
ID ADS20334 standard; protein; 268 AA.

AC ADS20334;

DT 18-NOV-2004 (first entry)

DE Fibroblast growth factor-5.

XX immunogenic peptide; fibroblast growth factor-5; FGF-5;
KW renal cell carcinoma-associated antigen; immune response; tumour;
KW antibody; antigen; human leukocyte antigen-A2; HLA-A2;
KW renal cell carcinoma; adenocarcinoma.

XX Homo sapiens.

XX MO2004045555-A2.

PD 03-JUN-2004.

PF 19-NOV-2003; 2003WO-US037065.

PR 19-NOV-2002; 2002US-0427920P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Hanada K, Yang JC, Perry-Lalley D;

DR WPI: 2004-431803/40.
DR N-PSDB: ADS20333.
DR GENBANK: AAB06463.
XX
PT New human leukocyte antigen (HLA)-A3 and HLA-A2 epitopes of fibroblast
PT growth factor-5 (FGF-5) for eliciting an immune response in a subject or
PT for treating an FGF-5 expressing tumor, e.g. renal cell carcinoma.
XX
PS Example 1, SEQ ID NO 16, 89pp; English.
XX
CC This sequence represents fibroblast growth factor-5 (FGF-5). FGF-5 is a
CC renal cell carcinoma-associated antigen. Peptide fragments derived from
CC FGF-5 were used to elicit an immune response in a subject, by
CC administering to a subject a first dose of a therapeutic amount of the
CC peptide. They may also be used for treating a FGF-5 expressing tumor in
CC a subject and for generating antibodies specific for an FGF-5 antigen. In
CC eliciting an immune response in a subject, the immune response elicited
CC is against an FGF-5 human leukocyte antigen (HLA)-A2 epitope, and the
CC peptide comprising ADS20325 is administered resulting in elicitation of
CC the immune response against the FGF-5 HLA-A2 epitope. The method elicits
CC an immune response against a renal cell carcinoma. The subject has an FGF
CC -5 expressing tumor, particularly an adenocarcinoma or renal cell
CC carcinoma.
XX
SQ Sequence 268 AA;
Query Match 100.0%; Score 268; DB 8; Length 268;
Best Local Similarity 100.0%; Pred. No. 8, 6e-250;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSFLLLPFSLILISAWHGKRLAPGQPPAATDNRPIGSSSSSSAMSSSSAS 60
DB 1 MSLSFLLLPFSLILISAWHGKRLAPGQPPAATDNRPIGSSSSSSAMSSSSAS 60
QY 61 SSPASISGSGSLGQSSFGWSPSGRRTSLYCRVGIQYIPDGKNGSHEANL 120
DB 61 SSPASISGSGSLGQSSFGWSPSGRRTSLYCRVGIQYIPDGKNGSHEANL 120
QY 121 LRIPAVSQGIYGVFNSNFKLMSKKGKILHASAKFTDDCKFRERPOENSNTYASAIHR 180
DB 121 LRIPAVSQGIYGVFNSNFKLMSKKGKILHASAKFTDDCKFRERPOENSNTYASAIHR 180
QY 181 TETGTGEWYVALNKRKAKRGCSPRVYKQHIISTHPLPRFQSQPPLSFVTVPEKKNP 240
DB 181 TETGTGEWYVALNKRKAKRGCSPRVYKQHIISTHPLPRFQSQPPLSFVTVPEKKNP 240
QY 241 SPIKSKTLPISAPRKNTNSVYKRLKFRFG 268
DB 241 SPIKSKTLPISAPRKNTNSVYKRLKFRFG 268
RESULT 14
AAE00639
ID AAE00639 standard; peptide; 246 AA.
XX
AC AAE00639;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human fibroblast growth factor-5 (FGF-5) peptide #1 from clone 6A4-1.
XX
KW Human; fibroblast growth factor-5; FGF-5; neoplasm; cytostatic; RCC;
KW renal cell carcinoma; immunomodulator; gene therapy; carcinoma; breast;
KW prostate; bladder; pancreas; TAA; tumor associated antigen;
KW horseshoe kidney; Hipel-Lindau disease; acquired renal cystic disease;
KW adult polycystic kidney disease; clone 6A4-1.
XX
OS Homo sapiens.
XX
OS
XX
PN WO200125271-A2.
XX
PD 12-APR-2001.
XX

PF 29-SEP-2000; 2000WO-US026689.
XX
XX 02-OCT-1999; 99US-0157103P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PA Handa K, Yang JC;
XX
PI
XX
DR WPI: 2001-290607/30.
DR N-PSDB: AAD03937.
XX
PT Treating a subject having a neoplasm expressing fibroblast growth factor-
PT 5 (FGF-5), e.g. prostate, breast, bladder, or pancreas carcinoma.
PT comprises modulating an immune response to FGF-5 or modulating FGF-5
PT expression or activity.
XX
PS Claim 7, Page 92, 101pp; English.
XX
CC The present invention relates to a method for treating a subject having
CC neoplasm expressing fibroblast growth factor-5 (FGF-5) comprising
CC modulating an immune response to FGF-5 or FGF-5 expression or activity.
CC FGF-5 is a tumor associated antigen (TAA). The method is useful for
CC treating or preventing a neoplasm such as prostate carcinoma, breast
CC carcinoma (RCC) and diseases such as Hipel-Lindau disease, horseshoe
CC kidneys, adult polycystic kidney disease and acquired renal cystic
CC disease. FGF-5 polypeptides may be used as immunogen in the production of
CC antibodies, which are useful in quantitative immunoassays that determine
CC concentrations of antigen-bearing substances in biological samples, and
CC to (semi-)quantitatively identify the presence of antigen in a biological
CC sample. The antibodies may also be used to treat FGF-5 expressing or
CC overexpressing tumours by decreasing FGF-5 activity, as diagnostic agents
CC to monitor the progression or regression of an FGF-5 expressing or
CC overexpressing tumour in a patient undergoing therapy for the treatment
CC of neoplasm. FGF-5 cDNA is also useful in gene therapy. The present
CC sequence is a human FGF-5 peptide from clone 6A4-1
XX
SQ Sequence 246 AA;
Query Match 91.8%; Score 246; DB 4; Length 246;
Best Local Similarity 100.0%; Pred. No. 1, 4e-228;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 EKRLAPKQPPAATDNRPIGSSSSSSAMSSSSASPPASISGSGSLGQSSFGWS 82
DB 1 EKRLAPKQPPAATDNRPIGSSSSSSAMSSSSASPPASISGSGSLGQSSFGWS 60
QY 83 PSGRRTGSLYCRVGIQYIPDGKNGSHEANL 142
DB 61 PSGRRTGSLYCRVGIQYIPDGKNGSHEANL 120
QY 143 AMSKKGKILHASAKFTDDCKFRERPOENSNTYASAIHRTKTKREWYVALNKRKAKRG 202
DB 121 AMSKKGKILHASAKFTDDCKFRERPOENSNTYASAIHRTKTKREWYVALNKRKAKRG 180
QY 203 SPRVYKQHIISTHPLPRFQSQPPLSFVTVPEKKNPSPISKPLPSAPRKNTNSVKR 262
DB 181 SPRVYKQHIISTHPLPRFQSQPPLSFVTVPEKKNPSPISKPLPSAPRKNTNSVKR 240
QY 263 LKFRFG 268
DB 241 LKFRFG 246
RESULT 15
AAV31793
ID AAV31793 standard; protein; 247 AA.
XX
XX AAV31793;
XX
AC
XX
DT 06-DEC-1999 (first entry)
XX
DE Human fibroblast growth factor 5 mature polypeptide.
XX

